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OM protein - protein search, using sw model
Run on: August 4, 2003, 15:03:04 ; Search time 29 Seconds
(without alignments)

Title: US-10-016-768a-2
Perfect score: 273
Sequence: 1 KQPRKKRGRYRQYDHEIME..... KAOQIYGVPHSTLEYKVKER 53

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6C_PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/backfiles1.pep: *
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	59	21.6	191	2	US-08-286-819A-21	Sequence 21, Appl
2	59	21.6	191	3	US-08-980-357-21	Sequence 21, Appl
3	57	20.9	102	4	US-09-732-210-1293	Sequence 1293, AP
4	56	20.5	696	4	US-09-107-532A-6133	Sequence 6133, AP
5	55	20.3	104	4	US-09-732-210-1272	Sequence 1272, AP
6	54	19.8	625	4	US-09-252-991A-33087	Sequence 33087, AP
7	53.5	19.6	187	4	US-09-328-352-5117	Sequence 5117, AP
8	53.5	19.6	438	4	US-09-134-001C-3634	Sequence 3634, AP
9	53	19.4	137	4	US-09-107-532A-4469	Sequence 4469, AP
10	53	19.4	227	4	US-09-308-003-48	Sequence 48, Appl
11	53	19.4	390	4	US-09-303-12	Sequence 12, Appl
12	52.5	19.2	389	4	US-09-250-991A-24471	Sequence 24471, AP
13	52.5	19.2	810	4	US-09-540-804-25	Sequence 25, Appl
14	52	19.0	348	2	US-09-974-546-1	Sequence 546, AP
15	52	19.0	552	4	US-09-441-301A-4	Sequence 4, Appl
16	52	19.0	552	4	US-09-099-332-4	Sequence 4, Appl
17	52	19.0	560	4	US-09-446-301A-50	Sequence 50, Appl
18	52	19.0	663	1	US-07-912-015-2	Sequence 2, Appl
19	51.5	18.9	349	3	US-08-462-467B-18	Sequence 18, Appl
20	51.5	18.9	554	3	US-08-462-467B-22	Sequence 22, Appl
21	51.5	18.9	1399	3	US-08-462-467B-14	Sequence 14, Appl
22	51	18.7	101	4	US-09-732-210-1268	Sequence 1268, AP
23	51	18.7	218	4	US-09-107-532A-5919	Sequence 5919, AP
24	51	18.7	222	4	US-09-252-991A-20670	Sequence 20670, AP
25	51	18.7	425	3	US-08-462-467B-16	Sequence 16, Appl
26	51	18.7	649	3	US-08-462-467B-20	Sequence 20, Appl
27	51	18.7	1495	3	US-08-462-467B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-286-819A-21
Sequence 21, Application US/08286819A
; Patent No. 5871910
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-VALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
; IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; STREET: 1155 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286, 819A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/917, 146
; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NO. 5871910man F.
; REGISTRATION NUMBER: 24, 618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEX: 248855 OPAT UR
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 191 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-286-819A-21

RESULT 2
 US-08-980-357-21
 Sequence 21, Application US/0890357
 GENERAL INFORMATION:
 Patent No. 6013508
 APPLICANT: ARTHUR, MICHEL
 APPLICANT: DUTKA-MALEN, SYLVIE
 APPLICANT: MOLINAS, CATHERINE
 APPLICANT: COURVALIN, PATRICE
 TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
 TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPITIDES, IN PARTICULAR
 TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
 TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/980,357
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/4286,819
 FILING DATE: 05-AUG-1994
 FILING DATE: 08/174,582
 FILING DATE: 28-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/917,146
 FILING DATE: 10-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR/91/00855
 FILING DATE: 29-OCT-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 9013579
 FILING DATE: 31-OCT-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Oblon, No. 6013508man F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 660-060-0 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 413-3000
 TELEFAX: (703) 413-2220

Query Match 21 6%; Score 59; DB 2; Length 191;
 Best Local Similarity 29.6%; Pred. No. 0.71;
 Matches 16; Conservative 13; Mismatches 23; Indels 2; Gaps 1;
 QY 1 KOPRKKRGRRQY-DHEIMEEAIAVMSKMSVSKAQGTYGVPHSTLEYKVKE 52
 Db 135 KKEGKFKGRLKLYKHNHAGMYAVKLYKEGNTVQICEITNVSRLYRKLE 188
 US-08-980-357-21

RESULT 3
 US-08-732-210-1293
 Sequence 1293, Application US/09732210
 Patent No. 6573351
 GENERAL INFORMATION:
 APPLICANT: Bunkers, Greg J.
 APPLICANT: Liang, Jihong
 APPLICANT: Mittanck, Cindy A.
 APPLICANT: Seale, Jeffrey W.
 APPLICANT: Wu, Yonnie S.
 TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 FILE REFERENCE: 38-21(1506)B
 CURRENT APPLICATION NUMBER: US/09/732,210
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,513
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: US 60/169,340
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 1753
 SEQ ID NO 1293
 LENGTH: 102
 TYPE: PRT
 ORGANISM: Thermotoga maritima
 US-08-732-210-1293

RESULT 4
 US-08-107-532A-6133
 Sequence 6133, Application US/09107532A
 Patent No. 6583275
 GENERAL INFORMATION:
 APPLICANT: Lynn A. Doucette-Stamm and David Bush
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO
 NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02454
 COMPUTER READABLE FORM:
 MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 PRIOR FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ariniello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 6133:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 695 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (B) LOCATION 1...396
 SEQUENCE DESCRIPTION: SEQ ID NO: 6133:

Query Match 20.5%; Score 56; DB 4; Length 695;
 Best Local Similarity 32.1%; Pred. No. 11; Gaps 3;
 Matches 18; Conservative 8; Mismatches 18; Indels 12; Gaps 3;

Qy 3 PRKKRGYQYDHEIMEAIAMVMSGKMSVSKAQGIVGVPHSTLEYKV---KER 53
 Db 372 PTENARYERKLSNE--ERRKY---QMTVSRLGLFAOPHKVQSTKVVTEFGKER 420

RESULT 5
 US-09-732-210-1272
 Sequence 172; Application US/09732210
 Patent No. 6573361
 GENERAL INFORMATION:
 APPLICANT: Bunkers, Greg J.
 APPLICANT: Liang, Jihong
 APPLICANT: Mittanck, Cindy A.
 APPLICANT: Seale, Jeffrey W.
 APPLICANT: Wu, Yonnie S.
 TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
 FILE REFERENCE: 38-21(1536)B
 CURRENT APPLICATION NUMBER: US/09/732,210
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: US 60/169,513
 PRIOR FILING DATE: 1999-12-07
 PRIOR APPLICATION NUMBER: US 60/169,340
 PRIOR FILING DATE: 1999-12-07
 NUMBER OF SEQ ID NOS: 1753
 SEQ ID NO 1272
 LENGTH: 104
 TYPE: PRT
 ORGANISM: Helicobacter pylori

Query Match 20.3%; Score 55.5; DB 4; Length 104;
 Best Local Similarity 29.8%; Pred. No. 1.1; Gaps 1;
 Matches 14; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

Qy 5 KKRGRYQYDHEIMEA-IAVVMSGKMSVSKAQGIVGVPHSTLEYKV 50
 Db 1 | : | : | | : | : | | : | | : | |
 3 KIRLKAYDHVLDRSVAIVEAVKRSGSEERGPIPLPTKKNKRYTV 49

RESULT 6
 US-09-252-991A-33087
 Sequence 33087; Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 33087
 LENGTH: 625
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

Query Match 19.8%; Score 54; DB 4; Length 625;
 Best Local Similarity 36.1%; Pred. No. 18; Gaps 1;
 Matches 13; Conservative 7; Mismatches 12; Indels 4; Gaps 1;

Qy 6 KRGYRYQ---YDHIMEEAIAMVMSGKMSVSKAQG 37
 Db 90 ERGHHRQLGIAFOHEVAEEARAEAPVGRUAEQLAEG 125

RESULT 7
 US-09-320-352-5117
 Sequence 5117; Application US/0928352
 Patent No. 6562958
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 FILE REFERENCE: GTC98-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 5117
 LENGTH: 187
 TYPE: PRT
 ORGANISM: Acinetobacter baumannii

Query Match 19.6%; Score 53.5; DB 4; Length 187;
 Best Local Similarity 31.2%; Pred. No. 4.5; Gaps 2;
 Matches 15; Conservative 12; Mismatches 16; Indels 5; Gaps 1;

Qy 10 YRQYDHIMEEAIAMVMSGKMSVSKAQGIVGVPHSTLEYKV 52
 Db 64 YQRNNEIEKIEVNLFLK1SDSIKKLKG1DQTLGKNSSEDFKTE 111

RESULT 8
 US-09-114-001C-3634
 Sequence 3634; Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
 TITLE OF INVENTION: EPIDERMIOSIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60,064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3634

; LENGTH: 438

; TYPE: PRT

; ORGANISM: *Staphylococcus epidermidis*

; Query Match 19.6%; Score 53.5; DB 4; Length 438;

; Best Local Similarity 38.2%; Pred. No. 14; Mismatches 5; Indels 11; Gaps 1;

; Matches 13; Conservative 5; Mismatches 5; Indels 11; Gaps 1;

; QY 4 RKKRGYRQYH-----EIMPEAIAWMV 26

; Db 129 RKKRGYRQYH-----MSGKMSVSKAQGIVGVPHSTLEYK 162

; RESULT 9

; US-09-107-532A-4469

; Sequence 4469 Application US/09107532A

; Patent No. 638325

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 024354

; COMPUTER READABLE FORM: MEDIUM TYPE: CD-ROM 1S09660

; COMPUTER: PC OPERATING SYSTEM: <Unknown>

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107-532A

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Arinello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-8277

; INFORMATION FOR SEQ ID NO: 4469:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 137 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: *Enterococcus faecium*

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (B) LOCATION 1..137

; SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

; US-09-107-532A-4469

; Db 66 QKIRIRKAYEHRILQDOSADKIVETAKRTGASVSGPPIPLPTERSLYTIRATHKYK 121

; RESULT 10

; US-09-308-003-48

; Sequence 48 Application US/09308003

; Patent No. 6326170

; GENERAL INFORMATION:

; APPLICANT: Burnham, Martin K. R.

; APPLICANT: Lonetto, Michael A.

; APPLICANT: Warren, Patrick V.

; TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES, POLYPEPTIDES AND THEIR USES

; FILE REFERENCE: GM10053

; CURRENT APPLICATION NUMBER: US/09/308,003

; CURRENT FILING DATE: 1999-05-10

; EARLIER APPLICATION NUMBER: 60/058,710

; EARLIER FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: FastSEQ for Windows Version 3.0

; LENGTH: 227

; QY 12 QYDH-----EIMPEAIAWMVMSGKMSVSKAQGIVGVPHSTLEYK 49

; Db 49 KYDYARSGNPNRELLEKARLEGKFAFAFASGIAIAISAVLIFK 94

; RESULT 11

; US-09-308-003-12

; Sequence 12, Application US/09308003

; Patent No. 6326170

; GENERAL INFORMATION:

; APPLICANT: Burnham, Martin K. R.

; APPLICANT: Lonetto, Michael A.

; APPLICANT: Warren, Patrick V.

; TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES, POLYPEPTIDES AND THEIR USES

; FILE REFERENCE: GM10093

; CURRENT APPLICATION NUMBER: US/09/308,003

; CURRENT FILING DATE: 1999-05-10

; EARLIER APPLICATION NUMBER: 60/058,710

; EARLIER FILING DATE: 1997-09-12

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: FastSEQ for Windows Version 3.0

; LENGTH: 390

; SEQ ID NO 12

; TYPE: PRT

; ORGANISM: *Staphylococcus aureus*

; RESULT 12

; US-09-308-003-12

; Query Match 19.4%; Score 53; DB 4; Length 390;

; Best Local Similarity 28.3%; Pred. No. 14; Mismatches 15; Indels 8; Gaps 1;

; Matches 13; Conservative 10; Mismatches 15; Indels 8; Gaps 1;

; QY 12 QYDH-----EIMPEAIAWMVMSGKMSVSKAQGIVGVPHSTLEYK 49

; Db 42 KYDYARSGNPNRELLEKARLEGKFAFAFASGIAIAISAVLIFK 87

; Query Match 19.4%; Score 53; DB 4; Length 137;

; Best Local Similarity 21.4%; Pred. No. 3.5; Mismatches 18; Indels 10; Gaps 1;

; Matches 12; Conservative 16; Mismatches 18; Indels 10; Gaps 1;

; QY 4 RKKRGYRQYH-----MSGKMSVSKAQGIVGVPHSTLEYK 49

; Db 129 RKKRGYRQYH-----RKKRGYRQYH-----MSGKMSVSKAQGIVGVPHSTLEYK 49

; APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIORITY NUMBER: US 60/074, 788
 PRIORITY FILING DATE: 1998-02-18
 PRIORITY FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 24471
 LENGTH: 389
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 US-09-252, 991A-24471

Query Match 19.2%; Score 52.5; DB 4; Length 389;
 Best Local Similarity 22.8%; Pred. No. 16; Mismatches 16; Indels 13; Gaps 2;
 Matches 13; Conservative 15; Mismatches 16; Indels 13; Gaps 2;
 Qy 8 GRYGYDHEIMEEATA-----MVGSKMSVSKAQGIVGVPHSTLEYKVER 53
 Db 217 GEFQOGAHEADRAVQAQWRILLEEVEDVVAAGEAGIAASDQHY--PHSRIGLRLQ 271.

RESULT 13

US-09-540-824-25

Sequence 25, Application US/09540824

Patent No. 6383753

GENERAL INFORMATION:

APPLICANT: Thiele, Dennis

APPLICANT: Liu, Phillip

TITLE OF INVENTION: No. 6383753el Yeast and Mammalian Regulators of Cell Proliferation

FILE REFERENCE: US-04266

CURRENT APPLICATION NUMBER: US/09/540, 824

CURRENT FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO: 25

LENGTH: 810

TYPE: PRT

ORGANISM: *Saccharomyces cerevisiae*

US-09-540-824-25

Query Match 19.2%; Score 52.5; DB 4; Length 810;
 Best Local Similarity 36.8%; Pred. No. 42; Mismatches 7; Indels 12; Gaps 5; Gaps 1;
 Matches 14; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

Qy 1 KOPRKRRGRQYDHEIMEEAIAAMVMSGKAVSKAQGIVGVPHSTLEYKVER 38
 Db 199 QQPQRKTK----AEVMKEVIASKSKFYKQEROQG 231

RESULT 14

US-08-974-546-1

Sequence 1, Application US/08974546

Patent No. 5945287

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Lal, Preeti

APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvi

TITLE OF INVENTION: TWO HUMAN HEAT SHOCK PROTEIN HOMOLOGS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974, 546

FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILE REFERENCE: 04266

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PR-0428

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-955-0555

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 348 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: BRAUTUT21

CLOSE: 2525691

US-08-974-546-1

Query Match 19.0%; Score 52; DB 2; Length 348;
 Best Local Similarity 39.0%; Pred. No. 17; Mismatches 4; Indels 19; Gaps 2; Gaps 1;
 Matches 16; Conservative 39.0%; Pred. No. 17; Mismatches 4; Indels 19; Gaps 2; Gaps 1;

Qy 5 KKRGRYDHEIMEEAIAAMVMSGKAVSKAQGIVGVPHSTLEYKVER 45
 Db 59 KKRGLYDQYGEGLKIGGG--TSGGSSGFHITFHDPHAT 97

RESULT 15

US-09-446-301A-4

Sequence 4, Application US/09446301A

Patent No. 6506893

GENERAL INFORMATION:

APPLICANT: EL SOLH, NEVINE

APPLICANT: ALLINET, JEANINE

TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE

TITLE OF INVENTION: TO STREPTOCIN A OR TO STREPTOCIN B AND RELATED

TITLE OF INVENTION: COMPOUNDS

FILE REFERENCE: 03715-0059

CURRENT APPLICATION NUMBER: US/09/446, 301A

CURRENT FILING DATE: 1999-12-20

NUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin ver. 2.1

SEQ ID NO: 4

LENGTH: 552

TYPE: PRT

ORGANISM: *Staphylococcus sp.*

US-09-446-301A-4

Query Match 19.0%; Score 52; DB 4; Length 552;
 Best Local Similarity 31.1%; Pred. No. 30; Mismatches 14; Conservative 31.1%; Pred. No. 30; Mismatches 11; Indels 12; Gaps 8; Gaps 2;

Qy 4 RKKRGRYDHEIMEEAIAAMVMSGKMSVSKAQGIVGVPHSTLEYKVER 46
 Db 193 RKQQEYEVNSKRKLEQAI----KLKENKAQGMIKPSKT 231

Search completed: August 4, 2003, 15:08:06
 Job time: 30 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2003, 14:55:14 ; Search time 26 Seconds
(without alignments)
95.862 Million cell updates/sec

Title: US-10-016-768a-2

Perfect score: 273

Sequence: 1 KQPRKKRGRYRQYDHEIMEE.....KAOQIYGVPHSTLEYKVKER 53

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt;41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.5	25.5	753	1 TKR_DROME	P14083 drosophila
2	63	23.1	977	1 BABL_DROME	Q9w0k7 drosophila
3	61	22.3	352	1 YFDF_ECOLI	P76505 escherichia
4	59	21.6	191	1 TNRC_ENTRC	Q06237 enterococcus
5	58	21.2	1067	1 BAB2_DROME	Q9w0k4 drosophila
6	58	21.2	342	1 RECL_MYXXA	P48291 myxococcus
7	58	21.2	397	1 CISH_SYN13	Q99777 synechocyst
8	57	20.9	1	1 RS10_THEME	P38518 thermocyst
9	56.5	20.7	364	1 SYW_METTH	Q26352 methanobact
10	56	20.5	102	1 RS10_LACIAC	Q9cwl1 lactococcus
11	56	20.5	102	1 RS10_LISMO	Q927k6 listeria mo
12	55.5	20.3	104	1 RS10_HELEY	P56017 helicobacte
13	55	20.3	169	1 Y7689_METUA	Q81719 methanococc
14	55	20.1	236	1 Y416_CHLTR	Q84421 chlamydiate
15	55	20.1	420	1 SYH_STAAM	Q32422 staphylococ
16	55	20.1	765	1 PUR1_ARC6U	Q82833 archaeoglob
17	55	20.1	809	1 QUITA_ACICA	Q59086 acinetobact
18	55	20.1	882	1 ALKS_PSEOL	P17051 pseudomonas
19	54	20.0	2607	1 BAB2_BACLI	Q88007 bacillus 11
20	54	19.8	352	1 RECA_BORRE	P37740 bordetellla
21	54	19.8	764	1 METE_SCBPO	Q9t19g schizosacch
22	54	19.8	936	1 FHL11_YEAST	P39521 saccharomy
23	54	19.8	1220	1 DP3A_THEQO	Q9xdh5 thermus aqu
24	54	19.8	1347	1 TOP2_BOMMO	Q16140 bombyx mori
25	53.5	19.6	138	1 YFFO_ECOLI	P76546 escherichia
26	53.5	19.6	258	1 BPHF_RHOSO	Q05151 rhodococcus
27	53.5	19.6	375	1 Y785_MEHTA	Q58195 methanococc
28	53.5	19.6	714	1 PUR1_METH	Q27427 methanobact
29	53	19.4	102	1 RS10_BACID	Q92915 bacillus ha
30	53	19.4	102	1 RS10_STRCO	Q910e1 streptomyce
31	52.5	19.2	344	1 CHER_CAUCR	Q87717 caulobacter
32	52.5	19.2	478	1 FXD2_HUMAN	Q9juj5 homo sapien
33	52.5	19.2	1390	1 N155_RAT	P37199 rattus norv

ALIGNMENTS

RESULT 1

ID TKR_DROME STANDARD PRT: 753 AA.

AC P14083; DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Protein TKR.

GN DR
RA Drosophila melanogaster (Fruit fly)
RA Eukaryota; Metazoa; Arthropoda; Hexapoda; Brachycera; Muscomorpha;
RA Neoptera; Endopterygota; Diptera; Drosophilidae; Drosophila;
RA Ephydriidae; Drosophilidae; Drosophila;
RA NCI_TAXID=7277;
RN [1]

RP SEQUENCE FROM N.A.
RA Haller J., Cote S., Broenner G., Jaekle H.;
RA "Dorsal and neural expression of a tyrosine kinase-related Drosophila gene during embryonic development.";
RA Genes Dev. 1:862-867(1987).

RL CC
CC -!- FUNCTION: POSSIBLE REGULATORY ROLE DURING DEVELOPMENT.
CC -!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A KINASE ON THE BASIS OF WEAK AND NON-SIGNIFICATIVE SIMILARITIES.

DR PIR: A27041; A27041;
DR FlyBase: FBgn003715; Tkr.
DR Pfam; PF05225; HTH_Psq; I.
FT DOMAIN 143 151 POLY-ASP-POLY-GLU.
FT DOMAIN 153 157 POLY-ALA.
FT DOMAIN 174 183 POLY-ASN.
FT DOMAIN 221 224 POLY-ASN.
FT DOMAIN 297 306 POLY-ALA.
FT DOMAIN 325 332 POLY-ALA.
FT DOMAIN 709 712 POLY-ALA.
SQ SEQUENCE 753 AA: F98D3272A7DDBE5E CRC64;

Query Match 25.5%; Score 69.5; DB 1; Length 753; Best Local Similarity 32.1%; Pred. No. 0.31; Matches 17; Conservative 12; Mismatches 17; Indels 7; Gaps 1; Qy 1 KQPRKK-----RGRYRQYDHEIMEAATAMVMSGKMSVKAQIYGVPHSTL 46 Db 496 KMPEPKQHSAPRGGPPSPWNTELAQHVNKKMTSQASRIFGPYNL 548

RESULT 2

ID BAB1_DROME STANDARD PRT: 977 AA.

AC Q9w0k7; 023368; Q8MR78; Q9UJH7; DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE BAB1_OR_BAB OS RCG5097/CG13910.
OS Drosophila melanogaster (Fruit fly)
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC	RX
OC	RA
Ephydriodea; Drosophilidae; Drosophila.	Stapleton M., Carlson J.W., Brookstein P., Yu C., Champe M.,
NCBI_TAXID=7227;	Rubin G.M., Celniker S.E., Champe M., Park S., Wan K.H.,
[1]	Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8 (2002).
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TISSUE SPECIFICITY;	RN
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Couderc J.L., Godt D., Zollman S., Chen J., Li M., Tiang S.,	RA
Cranton S.E., Sahut-Barnola I., Laski F.A.;	RA
"The bric a brac locus consists of two paralogous genes encoding	RA
BTB/POZ domain proteins and acts as a homeotic and morphogenetic	RT
regulator of imaginal development in <i>Drosophila</i> .";	RT
Development 129:2419-2433 (2002).	RL
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STRAIN=Berkeley;	RX
MEDLINE=20196006; PubMed=10731132;	RX
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	RA
Amanatides P.G., Scherer S.E., Li P.W., Hawkins R.A., Galle R.F.,	RA
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	RA
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,	RA
Branden R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	RA
Wan K.H., Dorele C., Baxter E.G., Heitz G., Nelson C.R., Miklos G.L.G.,	RA
Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	RA
Bailey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	RA
Beeson K.Y., Benos P.V., Baxendale J., Bhandari D., Bolshakov S.,	RA
Borkova D., Botchan M.R., Bouck J., Brookstein P., Brottier P.,	RA
Burttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	RA
Cherry J.M., Cawley S., Dahliek C., Davenport L.B., Davies P.,	RA
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	RA
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	RA
Durbin R., Evans C.C., Ferrajoli A.E., Garg N.S., Gelbart W.M., Glasser K.,	RA
Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,	RA
Gloedk F., Gorrell J.H., Gu Z., Guan P., Harris M.,	RA
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,	RA
Hoskin D., Houston K.A., Howard T.J., Wei M.-H., Ibegwam C.,	RA
Jahali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	RA
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	RA
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	RA
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	RA
Merkulov G., Milshina N.V., Nobarry C., Morris J., Mosherei A.,	RA
Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,	RA
Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacleb J.M.,	RA
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	RA
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shien H.,	RA
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,	RA
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	RA
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	RA
Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,	RA
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	RA
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	RA
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	RA
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,	RA
"The genome sequence of <i>Drosophila melanogaster</i> .";	RL
Science 287:2185-2195 (2000).	RL
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Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a	RT
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Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a	RT
systematic review.",	RT
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	RL
[4]	RN
SEQUENCE FROM N.A. (ISOFORM A).	RP
STRAIN=Berkeley; TISSUE=Testis;	RC
REVISIONS:	RX
STRAIN=Berkeley;	RX
MEDLINE=22426069; PubMed=12537572;	RX
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	RA
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	RA
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,	RA
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,	RA
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,	RA
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,	RA
Lewis S.E.,	RA
Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a	RT
systematic review.",	RT
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	RL
[4]	RN
SEQUENCE FROM N.A. (ISOFORM A).	RP
STRAIN=Berkeley; TISSUE=Testis;	RC
REVISIONS:	RX
STRAIN=Berkeley;	RX
MEDLINE=22426069; PubMed=12537572;	RX
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	RA
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	RA
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,	RA
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,	RA
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,	RA
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,	RA
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systematic review.",	RT
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	RL
[4]	RN
SEQUENCE FROM N.A. (ISOFORM A).	RP
STRAIN=Berkeley; TISSUE=Testis;	RC
REVISIONS:	RX
STRAIN=Berkeley;	RX
MEDLINE=22426069; PubMed=12537572;	RX
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	RA
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	RA
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,	RA
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,	RA
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,	RA
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,	RA
Lewis S.E.,	RA
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systematic review.",	RT
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	RL
[4]	RN
SEQUENCE FROM N.A. (ISOFORM A).	RP
STRAIN=Berkeley; TISSUE=Testis;	RC
REVISIONS:	RX
STRAIN=Berkeley;	RX
MEDLINE=22426069; PubMed=12537572;	RX
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	RA
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	RA
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Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,	RA
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Lewis S.E.,	RA
Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a	RT
systematic review.",	RT
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	RL
[4]	RN
SEQUENCE FROM N.A. (ISOFORM A).	RP
STRAIN=Berkeley; TISSUE=Testis;	RC
REVISIONS:	RX
STRAIN=Berkeley;	RX
MEDLINE=22426069; PubMed=12537572;	RX
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	RA
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,	RA
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,	RA
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,	RA
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,	RA
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,	RA
Lewis S.E.,	RA
Annotation of the <i>Drosophila melanogaster</i> euchromatic genome: a	RT
systematic review.",	RT
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).	RL
[4]	RN
SEQUENCE FROM N.A. (ISOFORM A).	RP
STRAIN=Berkeley; TISSUE=Testis;	RC
REVISIONS:	RX
STRAIN=Berkeley;	RX
MEDLINE=22426069; PubMed=12537572;	RX
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,	

Query	Match
DR EMBL: L40367; AAC3541000.1; -.	21.2%; Score 58; DB 1; Length 397;
DR PIR: A57364; A57354.	DR
DR HSSP; P26345; 1G19.	DR
DR HAMAP; MF_00268; -; 1.	DR
DR InterPro; IPR03593; AAA_ATPase.	DR
DR InterPro; IPR01553; RecA.	DR
DR Pfam: PF00154; recA; 1.	DR
DR PRINTS; PRO0142; RecA.	DR
DR PRODOM; PDD00229; RecA; 1.	DR
DR SMART; SM00382; AAA; 1.	DR
DR PROSITE; PS00021; RecA_1; 1.	DR
DR PROSITE; PS50162; RecA_2; 1.	DR
DR PROSITE; PS50163; RecA_3; 1.	DR
DR DNA_damage; DNA_recombination; SOS_response; ATP-binding; DNA-binding.	DR
DR NP_BIND; 68 75 ATP (BY SIMILARITY).	DR
DR SEQUENCE 342 AA; 36055 MW; 7F86B4F9F0B47E4 CRC64;	DR
Query Match 0y 7 RGRYRQDHDHETEEAIAAMVMSCKMSKMSKAQGTYGYP 42	DR
Best Local Similarity 33.3%; Score 58; DB 1; Length 342; Pred. No. 4.1; Mismatches 15; Indels 4; Gaps 1; Matches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0; DB 24 RGSVMTLGGEARQKAVAVIPSGSGVVRALGVGYP 59	DR
RESULT 7	DR
CISY_SYN3	DR
ID_CISY_SYN3	DR
STANDARD; PRT; 397 AA.	DR
AC 059977;	DR
DT 01-NOV-1997 (Rel. 35, Created)	DR
DT 01-NOV-1997 (Rel. 35, Last sequence update)	DR
DT 15-SEP-2003 (Rel. 42, Last annotation update)	DR
DE Citrate synthase (EC 2.3.3.1).	DR
GN GLTA OR SL0401.	DR
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.	DR
OC NCBI_TaxID:1148;	DR
RN [1]	DR
RP SEQUENCE FROM N.A.	DR
RC STRAIN=MSBB / DSM 3109;	DR
RX MEDLINE=95095941; PubMed=8002596;	DR
RX MEDLINE=99287316; PubMed=10360571;	DR
RX MEDLINE=99287316; PubMed=10360571;	DR
RX Nelson K.E., Bocchetta M., Cammarano P., Tiboni O.,	DR
RX Saengelantoni A.M., Bocchetta M., Cammarano P., Tiboni O.,	DR
RX "Phylogenetic depth of S10 and SPC operons: cloning and sequencing of	DR
RX a ribosomal protein gene cluster from the extremely thermophilic	DR
RX bacterium Thermotoga maritima.";	DR
RX J. Bacteriol. 176:7703-7710(1994).	DR
RN [2]	DR
RP SEQUENCE FROM N.A.	DR
RC STRAIN=MSBB / DSM 3109;	DR
RX MEDLINE=99287316; PubMed=10360571;	DR
RX McDonald L.L., Utterback T.R., Gill S.R., Gwinn M.L., Dodson R.J.,	DR
RX Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,	DR
RX McDaniel L.L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,	DR
RX Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,	DR
RX Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,	DR
RX Salzberg S.L., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,	DR
RX "Evidence for lateral gene transfer between Archaea and Bacteria from	DR
RX genome sequence of Thermotoga maritima.";	DR
RX Nature 399:323-329(1999).	DR
RT -- FUNCTION: Involved in the binding of tRNA to the ribosomes (By	DR
RT similarity).	DR
CC -1 SIMILARITY: BELONGS TO THE SL0P FAMILY OF RIBOSOMAL PROTEINS.	DR
CC	DR
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	DR
CC	DR
CC EMBL: 221677; CAA79761;	DR
CC EMBL: A500198; AAD365671; -.	DR
DR InterPro: IPR00573; S10_bact.	DR
DR PIR: S40187; S40187.	DR
DR TIGR: TM1501;	DR
DR HAMAP; MF_00308; -; 1.	DR
DR InterPro: IPR01848; Ribosomal_S10.	DR
DR InterPro: IPR00573; S10_bact.	DR
DR Pfam: PF00338; Ribosomal_S10; 1.	DR
DR PRINTS: PRO00971; RIBOSOMALST10.	DR
DR PRODOM; PDD0127; Ribosomal_S10; 1.	DR
DR TIGRFAMS: TIGR01049; rpsJ_bact; 1.	DR
DR PROSITE: PS00361; RIBOSOMAL_S10; 1.	DR
DR Ribosomal protein; Complete proteome.	DR
DR SEQUENCE 102 AA; 11637 MW; 4CB4D2667D7C7F7 CRC64;	DR
Query Match 0y 20.9%; Score 57; DB 1; Length 102; Best Local Similarity 26.8%; Pred. No. 1.4;	DR

RA Glaser P., Frangoul L., Buchrieser C., Rusniok C., Amend A., Rabin F., Berche P., Bloch K., Brandt P., Chakraborty T., RA Baduel F., Berche P., Bloch K., Brandt P., Chakraborty T., RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P., RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D., Jones L.-M., Kaelest U., Kreft J., Kuhn M., Kunst F., Kurapkat G., RA Madueno E., Maitourna A., Mata Vicente J., Ng E., Nedjari H., RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R., RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A., RA Vazquez-Boland J.-A., Voss H., Weiland J., Cossart P., RA RT RT RL Science 294:849-852(2001).
 -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (BY similarity).
 -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.

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 CC EMBL; AL596173; CAC98008.1; -.
 CC DR EMBL; AL591983; CAD00711.1; -.
 CC DR PIR; AH1779; AH1779.
 CC DR PIR; AL1403; AL1403.
 CC DR ListiList; LM002633; -.
 CC DR ListiList; LIN02782; -.
 CC DR HAMAP; MF_00508; -; 1.
 CC DR InterPro; IPR001848; Ribosomal_S10.
 CC DR Pfam; PF00338; Ribosomal_S10; 1.
 CC DR PRINTS; PR00571; RIBOSOMALS10.
 CC DR PRODOM; PD001272; Ribosomal_S10; 1.
 CC DR TIGRFAMS; TIGR01049; rpsJ_bact; 1.
 CC DR PROSITE; PS00361; RIBOSOMAL_S10; 1.
 CC KW Ribosomal protein; Complete proteome.
 CC SQ SEQUENCE 102 AA; 11682 MW; 7E4B186EA533CCDB CRC64;

Query Match 20.5%; Score 56; DB 1; Length 102; Best Local Similarity 25.0%; Pred. No. 1.9; Matches 14; Conservative 13; Mismatches 19; Indels 10; Gaps 1; Ov 4 RKKRGRGRYROYDHIMEEA1AMV-----MSGKMSVSKAOGIYGVPHSTLEYK 49 Db 4 QKIRIRKAYDHRILDQSAEKIVETAKRSGASVSGPIPILPTEKSIYVLRVAVHKY 59

RESULT 12

RS10_HELPY STANDARD: PRT; 104 AA.
 AC P56017;
 ID RS10_HELPY
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE SOS 1bposnal protein S10.
 GN RSJ OR HP1220 OR JHP1240.
 OS Helicobacter pylori (Campylobacter pylori), and Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Helicobacteraceae; Helicobacter.
 OC NCBI_TaxID=210, 85963;
 RN 1]
 RN Sequence from N.A.
 RN RC MEDLINE=26695 / ATCC 700392;
 RN RX MEDLINE=9734467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cottrell M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M., Ventier J.C.;
 RA "The complete genome sequence of the gastric pathogen Helicobacter pylori." Nature 388:539-547(1997).
 RN [2]
 RN SEQUENCE FROM N.A.
 RN RT STRAIN=J99;
 RN RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., de Jonge B.L., Carmel G., Tummolo P.J., Caruso A., Urias-Nickelsen M., Mills D.M., Ives C., Gibson R., Melberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., Trust T.J.;
 RA "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori." Nature 397:176-180(1999).
 RN -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (BY similarity).
 CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.

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 CC EMBL; AL5900633; AAD08359.1; -.
 CC DR EMBL; AF001547; AAD06791.1; -.
 CC DR PIR; H64684; H64684.
 CC DR TIGR; HP1320; -.
 CC DR HAMAP; MF_00508; -; 1.
 CC DR InterPro; IPR001848; Ribosomal_S10.
 CC DR InterPro; IPR00571; S10_bact.
 CC DR Pfam; PF00338; Ribosomal_S10; 1.
 CC DR PRINTS; PR00571; RIBOSOMALS10.
 CC DR PRODOM; PD001272; Ribosomal_S10; 1.
 CC DR TIGRFAMS; TIGR01049; rpsJ_bact; 1.
 CC DR PROSITE; PS00361; RIBOSOMAL_S10; 1.
 CC KW Ribosomal protein; Complete proteome.
 CC SQ SEQUENCE 104 AA; 11918 MW; 7E8A60A965B41CE1 CRC64;

Query Match 20.3%; Score 55.5; DB 1; Length 104; Best Local Similarity 20.8%; Pred. No. 2.2; Matches 14; Conservative 12; Mismatches 20; Indels 1; Gaps 1; Ov 5 KKRGRGRYROYDHIMEA1AMVMSGKMSVSKAOGIYGVPHSTLEYK 50 Db 3 KIRIRKAYDHRILDQSAEKIVETAKRSGASVSGPIPILPTEKSIYVLRVAVHKY 49

RESULT 13

Y769_MEJJA STANDARD: PRT; 169 AA.
 ID Y769_MEJJA
 AC 053179;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0769.
 GN M0769.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanococciidae; Methanococccaceae; Methanococccus; NCBI_TaxID=210;
 RN 1]
 RN Sequence from N.A.
 RN RC STRAIN=AL-1 / DSM 2661 / ATCC 43067;
 RN MEDLINE=96337999; PubMed=8688087;

RA Abdell-Neguied S.S.;
 RT "Cooperative structural dynamics and a novel fidelity mechanism in
 histidyl-tRNA synthetases.";
 RL Biochemistry 38:12206-12304 (1999);
 CC -!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
 CC diphosphate + L-histidyl-tRNA(His).
 CC -!- SUBUNIT: Homodimer (By similarity).
 CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 CC
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 CC
 DR EMBL; AP003363; BAB5793.1;
 CC DR EMBL; AP003134; BAB42723.1;
 DR EMBL; AP004827; BAB9546.1;
 DR EMBL; D76414; BAA23141.1;
 PIR: F89945;
 DR PDB: 1QBO; 26-SEP-01;
 DR HAMAP; MF_00127; 1;
 DR InterPro; IPR004154; HgTP_anticodon.
 DR InterPro; IPR004516; Hiss.
 DR InterPro; IPR002314; tRNA_synt_2b.
 DR InterPro; IPR006195; tRNA_ligase_II.
 DR InterPro; IPR03129; HgTP_anticodon; 1.
 DR Pfam; PF00587; tRNA_synt_2b; 1.
 DR TIGRFAMS; TIGR00442; Hiss; 1.
 DR PROSITE; PS0862; AA_TRNA_LIGASE_II; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 3D-structure; Complete proteome.
 FT DISULFID 191 194
 SQ SEQUENCE 420 AA; 48283 MW; 3B79531695278CA4 CRC64;

Query Match 20.1%; Score 55; DB 1; Length 420;
 Best Local Similarity 29.6%; Pred. No 13;
 Matches 16; Conservative 8; Mismatches 12; Indels 18; Gaps 2;
 Qy 4 RKKRGGRYROYDH-----EIMEEIAAMMSGKSVSKAQGIYGVPHSTL 46
 Db 115 RKQKGRYRQFNQFGVEATGAENPSVDAEVLMVHIXOS-----FGIKHLKL 161

Search completed: August 4, 2003, 15:05:02

Job time : 28 secs

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GenCore version 51.6
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OM protein - protein search, using sw model
Run on: August 4, 2003, 15:02:04 ; Search time 40 Seconds
Perfect score: 273

Title: US-10-016-768A-2
Sequence: KQPRKKRGRYRQDVHEIMEEATAMVMSGKMSVSKAOGIYGVPHSTLEYKVKER 53

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 95168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	163	59.7	185	hypothetical protein T01C1.3 - Caenorhabditis elegans
2	88.5	32.4	1085	hypothetical protein pipsqueak gene
3	69.5	753	2	Caenorhabditis elegans
4	61	22.3	352	hypothetical protein tyrosine kinase-receptor
5	59	21.6	191	hypothetical protein resolvase homolog
6	59	21.6	419	hypothetical protein
7	59	21.6	424	hypothetical protein recombinase
8	58	21.2	342	hypothetical protein synthase
9	58	21.2	397	hypothetical protein
10	58	21.2	1880	hypothetical protein
11	57.5	21.1	139	hypothetical protein
12	57.5	21.1	140	hypothetical protein
13	57	20.9	102	hypothetical protein
14	56.5	20.7	364	hypothetical protein
15	56.5	20.7	427	hypothetical protein
16	56	20.5	102	hypothetical protein
17	56	20.5	102	hypothetical protein
18	56	20.5	102	hypothetical protein
19	56	20.5	264	hypothetical protein
20	56	20.5	1692	hypothetical protein
21	55.5	20.3	104	hypothetical protein
22	55.5	20.3	169	hypothetical protein
23	55	20.1	114	hypothetical protein
24	55	20.1	236	hypothetical protein
25	55	20.1	415	hypothetical protein
26	55	20.1	420	hypothetical protein
27	55	20.1	765	hypothetical protein
28	55	20.1	809	hypothetical protein
29	54.5	20.0	204	hypothetical protein

RESULT 1

Query Match 59.7%; Score 163; DB 2; Length 185;

Best Local Similarity 56.6%; Pred. No. 2.4e-13; Matches 30; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 KOPRKKGGRYRQDVHEIMEEATAMVMSGKMSVSKAOGIYGVPHSTLEYKVKER 53

Db 83 KRSRPRKKRGRYRQDVHEIMEEATAMVMSGKMSVSKAOGIYGVPHSTLEYKVKER 135

RESULT 2

Query Match 59.7%; Score 163; DB 2; Length 185;

Best Local Similarity 56.6%; Pred. No. 2.4e-13; Matches 30; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 KOPRKKGGRYRQDVHEIMEEATAMVMSGKMSVSKAOGIYGVPHSTLEYKVKER 53

Db 83 KRSRPRKKRGRYRQDVHEIMEEATAMVMSGKMSVSKAOGIYGVPHSTLEYKVKER 135

Gene Pipsqueak protein A long form - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 23-Sep-2002

C;Accession: S66149; S66150; T45467

C;Weber, U.; Siegel, V.; Mlodzik, M.

EMBO J. 14, 6247-6257, 1995

A;Title: pipsqueak encodes a novel nuclear protein required downstream of seven-up f

A;Reference number: S66148; MUID:96134923; PMID:8557044

A;Accession: S66149

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1085 <WEB>

A;Cross-references: EMBL:X90986; NID:91149498; PIDN:CAA62474.1; PID:91149500

A;Accession: S66150

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1085 <WEB>

A;Cross-references: EMBL:X90985; NID:91149498; PIDN:CAA62475.1; PID:91149501

R;Horowitz, H.; Berg, C.A.

Development, 122, 1855-1871, 1996

ALIGMENTS

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
 A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
 A;Reference number: A71570; MUID:9900809; PMID:9784136
 A;Accession: F71488
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-1424 <ARN>
 A;Cross-references: GB:AE001335; GB:AE001273; NID:9332901; PIDN: AAC68825.1; PID:9332909
 A;Experimental source: serotype D, strain UW-3/CX
 C;Genetics:
 A;Gene: CT648
 C;Superfamily: Chlamydia hypothetical protein CT648
 Query Match 21.2%; Score 59; DB 2; Length 424;
 Best Local Similarity 32.7%; Pred. No. 13; Mismatches 17; Conservative 10; Mismatches 13; Indels 12; Gaps 3; Matches 17;
 Result 8
 QY 1 KOPKKRGRYRQDHEIMEEAIANVMSGK-----MSVSKAQGIVGVPH 43
 DB 232 KQGKLRSKYY--YD-PLTKEIACVNGKGKQVIYGVKAILETRQIVGVPH 280
 A57364 recombination protein recAa - Myxococcus xanthus
 N;Alternate names: recombinase A
 C;Species: Myxococcus xanthus
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 02-Feb-2001
 C;Accession: A57364
 R;Noriooka, N.; Hsu, M.Y.; Inouye, S.; Inouye, M.
 J;Bacteriol. 177, 4119-4182, 1995
 A;Title: Two recA genes in Myxococcus xanthus.
 A;Reference number: A57364; MUID:95332233; PMID:7608099
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-342 <RES>
 A;Cross-references: GB:L140367; NID:9848993; PIDN: AAC37000.1; PID:9848994
 C;Genetics:
 A;Gene: recA1
 C;Superfamily: recombination protein recA
 C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop; F68-75/Region: nucleotide-binding motif A (P-loop)
 F142-147/Region: nucleotide-binding motif B (P-loop)
 F74/Binding site: ATP (Lys) #status predicted
 Query Match 21.2%; Score 58; DB 2; Length 342;
 Best Local Similarity 33.3%; Pred. No. 14; Mismatches 12; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
 Result 9
 QY 7 RGRYRQDHEIMEEAIANVMSGKMSVSKAQGIVGVPH 42
 DB 24 RGSYNTLGEARSQKAVAVIPSSPGVGDRAILGVGYP 59
 A574344 citrate synthase gltA - Synechocystis sp. (strain PCC 6803)
 N;Alternate names: hypothetical protein sll0401
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
 C;Accession: S74344
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Ogi, K.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. A;Reference number: S74322; MUID:97051201; PMID:8905231
 A;Accession: S74344
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-397 <KAN>
 A;Cross-references: EMBL:D64001; GB:AB001339; NID:91001102; PIDN:BA10262.1; PID:9100
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Genetics:
 A;Gene: gltA
 A;Start codon: GTG
 C;Superfamily: citrate (si)-synthase
 Query Match 21.2%; Score 58; DB 2; Length 397;
 Best Local Similarity 35.0%; Pred. No. 16; Mismatches 14; Conservative 7; Mismatches 15; Indels 4; Gaps 1; Matches 17;
 Result 10
 QY 10 YRQDHEIMEEAIANVMSGKMSVSKAQGIVGVPHSTLEYK 49
 DB 3 YMMTDNEVFKEGLAGVPAAKSRVSHDGTGIG---LEYR 38
 A57361 tractin - medicinal leech
 C;Species: Hirudo medicinalis (medicinal leech)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
 C;Accession: T18531
 R;Huang, Y.; Jellies, J.; Johansen, K.M.; Johansen, J.
 J;Cell Biol. 138, 143-157, 1997
 A;Title: Differential glycosylation of tractin and leechCAM, two novel Ig-superfamily
 A;Reference number: Z18951; MUID:97362067; PMID:9214388
 A;Accession: T18531
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1880 <HUA>
 A;Cross-references: EMBL:U92813; NID:92275259; PID:92275260; PIDN: AAC47654.1
 A;Cross-references: GB:L140367; NID:9848993; PIDN: AAC37000.1; PID:9848994
 C;Genetics:
 A;Gene: recA1
 C;Superfamily: recombination protein recA
 C;Keywords: ATP; DNA binding; DNA recombination; DNA repair; nucleotide binding; P-loop; F68-75/Region: nucleotide-binding motif A (P-loop)
 F142-147/Region: nucleotide-binding motif B (P-loop)
 F74/Binding site: ATP (Lys) #status predicted
 Result 11
 QY 4 RKKRGRYRQDHEIMEEAIANVMSGKMSVSKAQGIVGVPH 42
 DB 889 RKRRSRSKNGNHDGVVIGHVTLNLPDSMVKAAVLVLNGKKGELESEPIFFYVPEGVPSKV 948
 A575179 hypothetical protein PAB2413 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-2000
 C;Accession: H75179
 R;anonymous, Genoscope
 A;Description: submitted to the EMBL Data Library, July 1999
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Reference number: A75001
 A;Molecule type: DNA
 A;Accession: H75179
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-139 <KAW>
 A;Cross-references: GB:AJ248284; GB:AL096836; NID:95457730; PIDN: CAB49519.1; PID:9545
 A;Experimental source: strain Orsay
 A;Genes: PAB2413
 C;Superfamily: Pyrococcus abyssi hypothetical protein PAB2413
 Query Match 21.1%; Score 57.5; DB 2; Length 139;
 Best Local Similarity 30.6%; Pred. No. 5; Mismatches 15; Conservative 12; Mismatches 21; Indels 1; Gaps 1;
 Result 12
 QY 5 KKRGRYRQDHEIMEEAIANVMSGKMSVSKAQGIVGVPHSTLEYK 53
 DB 85 KGRGRRRKSYKTLMMIEELKKGKTPREISDL-GIPIRTYLYLKK 132

RESULT 12
 H71033 hypothetical protein PH1560 - *Pyrococcus horikoshii*
 C;Species: *Pyrococcus horikoshii*
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
 C;Accession: H71033
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T
 ; Oiu, D.; Spadafora, R.; Vicaine, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivani, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfukui, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, *Pyrococcus horikoshii* H₁
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: H71033
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-140 <KAW>
 A;Cross-references: GB:AP000006; NID:93236133; PIDN:BAA30672.1; PID:93257989
 A;Experimental source: strain On3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH1560
 C;Superfamily: *Pyrococcus abyssi* hypothetical protein PAB2413

Qy	4 RKKRGGRYROYDHEIMEEATAMWMS- ::: ::: ::: ::: ::: :::	Oy	4 RKKRGGRYRYO---DHEIMEEATAMV---MSGMSVSKAOGTYGV ::: :: : :: : :: : :: :
Db	4 QKIRIKLKAYDHLLDESAKKIVAKTNSKVGPIPLPTERTLYCVRSPMKH 59	Db	125 RHOKGRYRQFTQDYEVLSADALNDAEAIALMVAVVOKLGLRGV 169
Query Match	20.9%; Score 57; DB 2; Length 102;	Query Match	20.7%; Score 56.5; DB 2; Length 427;
Best Local Similarity	26.8%; Pred. No. 4,7;保守性 15; Mismatches 14; Indels 17; Gaps 2;	Best Local Similarity	33.3%; Pred. No. 27;保守性 13; Mismatches 10; Indels 7; Gaps 2;
Matches	15; Conservative	Matches	15; Conservative
Qy	4 RKKRGGRYRYO---DHEIMEEATAMV---MSGMSVSKAOGTYGV ::: :: : :: : :: : :: :	Oy	4 RKKRGGRYRYO---DHEIMEEATAMV---MSGMSVSKAOGTYGV ::: :: : :: : :: : :: :
Db	125 RHOKGRYRQFTQDYEVLSADALNDAEAIALMVAVVOKLGLRGV 169	Db	125 RHOKGRYRQFTQDYEVLSADALNDAEAIALMVAVVOKLGLRGV 169
Search completed: August 4, 2003, 15:07:32	Search completed: August 4, 2003, 15:07:32	Search completed: August 4, 2003, 15:07:32	Search completed: August 4, 2003, 15:07:32
Job time : 43 secs	Job time : 43 secs	Job time : 43 secs	Job time : 43 secs

RESULT 14
E69131

GenCore version 5.1.5									
Copyright (c) 1993 - 2003 Compugen Ltd.									
OM protein - protein search, using sw model									
Run on: August 4, 2003, 14:54:34 ; Search time 83 seconds									
Result	No.	Score	Query	Match Length	DB ID	Description	Scoring table:	Sequence:	Title:
			Human E93 programm				BLOSUM62	US-10-016-768A-2	Perfect score: 273
1	273	100.0	53	23	AAE24592	Human E93 programm	Gapop 10.0 , Gapext 0.5	1 KOPRKKGGRYRYDHEIME. KAOQIYGVPHSILEVKYVER 53	Sequence: 1 KOPRKKGGRYRYDHEIME. KAOQIYGVPHSILEVKYVER 53
2	273	100.0	442	23	AAE24371	Human E93 programm			Scoring table: BLOSUM62
3	273	100.0	630	22	ABG1942	Novel human diagno			Scoring table: Gapop 10.0 , Gapext 0.5
4	234	85.7	104	23	ABP32451	Human ORF424 prot			Searched: 1107863 seqs, 158726573 residues
5	233.5	85.5	54	23	AEE24593	Fish E93 programme			Minimum DB seq length: 0
6	229	83.9	53	23	AEE24594	Mouse E93 programme			Maximum DB seq length: 200000000
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog			Post-processing: Minimum Match 0%
8	160	114.0	22	AAE71145	Drosophila melanog				Maximum Match: 100%
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog			Listing first: 45 summaries
SUMMARIES									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	RESULT 1		
2	273	100.0	442	23	AAE24371	Human E93 programm	ID AAE24592	standard; Protein: 53 AA.	
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	AC AAE24592;		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	DT 04-OCT-2002 (first entry)		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
ALIGNMENTS									
Result No. Score Query Match Length DB ID Description									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		
3	273	100.0	630	22	ABG1942	Novel human diagno	XX		
4	234	85.7	104	23	ABP32451	Human ORF424 prot	XX		
5	233.5	85.5	54	23	AEE24593	Fish E93 programme	PF 29-OCT-2001; 2001MO-US48053.		
6	229	83.9	53	23	AEE24594	Mouse E93 programme	XX		
7	165	60.4	53	23	AEE24370	Fruit fly E93 prog	PR 27-OCT-2000; 2000US-243865P.		
8	160	114.0	22	AAE71145	Drosophila melanog				
9	165	60.4	1165	23	AEE24372	Fruit fly E93 prog	XX		
RESULTS									
1	273	100.0	53	23	AAE24592	Human E93 programm	XX		
2	273	100.0	442	23	AAE24371	Human E93 programm	XX		

PI	Baehrecke EH;	XX	XX
XX		XX	PR
DR	WPI; 2002-479717/51.	XX	27-OCT-2000; 2000US-243865P.
XX		XX	PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
PT	Novel programmed cell death modulating proteins, useful for treating or preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction	XX	PI Baehrecke EH;
PT		XX	WPI; 2002-479717/51.
PS	Claim 1; Fig 1; 88pp; English.	XX	Novel programmed cell death modulating proteins, useful for treating or preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction
XX		XX	PT preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction
CC	The present invention relates to novel programmed cell death modulating proteins and polynucleotides encoding such proteins. Sequences of the invention are useful to screen potential cellular apoptosis inhibiting compounds to determine their use as therapeutic agents for treatment of diseases associated with increased programmed cell death. They are also useful for treating or preventing disorders associated with decrease in apoptosis. Programmed cell death modulating sequences are useful for treating or preventing cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma. Inhibition of the activity of the sequences of the invention are useful for treating disorders associated with increase in cell death or apoptosis such as acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g., Alzheimer's disease, retinitis pigmentosa, Parkinson's disease and cerebellar degeneration), ischaemic injuries (e.g., myocardial infarction, stroke, reperfusion injury), myelodysplastic syndromes (e.g., aplastic anaemia), toxin-induced diseases and other infectious or genetic immunodeficiencies. Sequences of the invention are used as vaccines and in gene therapy. The present sequence is human E93 programmed cell death modulating protein conserved domain.	CC	
CC		XX	CC The present invention relates to novel programmed cell death modulating proteins and polynucleotides encoding such proteins. Sequences of the invention are useful to screen potential cellular apoptosis inhibiting compounds to determine their use as therapeutic agents for treatment of diseases associated with increased programmed cell death. They are also useful for treating or preventing disorders associated with decrease in apoptosis. Programmed cell death modulating sequences are useful for treating or preventing cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma. Inhibition of the activity of the sequences of the invention are useful for treating disorders associated with increase in cell death or apoptosis such as acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g., Alzheimer's disease, retinitis pigmentosa, Parkinson's disease and cerebellar degeneration), ischaemic injuries (e.g., myocardial infarction, stroke, reperfusion injury), myelodysplastic syndromes (e.g., aplastic anaemia), toxin-induced diseases and other infectious or genetic immunodeficiencies. Sequences of the invention are used as vaccines and in gene therapy. The present sequence is human E93 programmed cell death modulating protein.
XX	Sequence 53 AA;	XX	CC
Query	Match 100.0%; Score 273; DB 23; Length 53;	Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC
Qy	1 KOPRKRRGRYQDYHIMEEIAMYMSGKMSVSKAQGIVGVPHSTLEYVKER 53	Db 1 KOPRKRRGRYQDYHIMEEIAMYMSGKMSVSKAQGIVGVPHSTLEYVKER 53	CC
RESULT 2		XX	CC
AAE24371		XX	CC
ID	AAE24371 standard; Protein: 442 AA.	AC	CC
AC	AAE24371;	XX	CC
XX	04-OCT-2002 (first entry)	AC	CC
DE	Human E93 programmed cell death modulating protein.	XX	CC
XX		XX	CC
KW	Human; cancer; programmed cell death modulating protein; adenocarcinoma; neurodegenerative disease; Alzheimer's disease; acquired immunodeficiency syndrome; AIDS; cellular apoptosis; leukaemia; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; myelodysplastic syndrome; cerebellar degeneration; Parkinson's disease; myeloma; aplastic anaemia; ischaemic injury; myocardial infarction; stroke; reperfusion injury; toxin-induced disease; genetic immunodeficiency; vaccine; gene therapy; lymphoma; cytotoxic; melanoma; neuroprotective; myeloma; nootropic; vasotropic; immunostimulant; cerebroprotective; cardiant; E93 protein.	XX	CC
KW		XX	CC
OS	Homo sapiens.	XX	CC
XX		XX	CC
FH	Key Location/Qualifiers	XX	CC
FT	Domain 353..405	XX	CC
FT	/note= "Conserved domain"	XX	CC
XX		XX	CC
PN	WO200234882-A2.	XX	31-MAR-2000; 2000US-0540217.
XX		XX	23-APR-2000; 2000US-0649167.
PD	02-MAY-2002.	XX	(HYSEQ-) HYSEQ INC.
XX		XX	PI Drmanac RT, Liu C, Tang YT;
PP	29-OCT-2001; 2001WO-US48053.	XX	

DR	WPI: 2001-639362/73.
XX	N-PSDB; AAS82129.
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
PT	Claim 20; SEQ ID No 48301; 103pp; English.
XX	CC
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, Oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abnormal protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic amino acid sequences or the invention.
CC	Note: The sequence data for this patent did not appear in the Printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences .
XX	SO
Query Match	100.0%; Score 273; DB 22; Length 630;
Best Local Similarity	100.0%; Pred. No. 6.4e-32;
Matches	53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KOPRKKRGRYRQYDHEIMEAIAAMVMSKMSVSKAQGIGYVPHSTLEYVKVER 53
Db	541 KOPRKKRGRYRQYDHEIMEAIAAMVMSKMSVSKAQGIGYVPHSTLEYVKVER 53
RESULT 4	
ABP32451	Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ID	ABP32451 standard; Protein: 104 AA.
AC	ABP32451;
XX	DT 09-JUL-2002 (first entry)
XX	DE Human ORF1424 protein, SEQ ID No:2848.
XX	Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haemopoiesis regulation; tissue growth; angiogenesis; activin; inhibitor; chemotactic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerability; vasoconstrictive; anti-ischaemic; anti-diabetic; cytosolic; non-specific; neuroprotective; anti-atherosclerotic; anti-coagulant; thrombolytic; cardiotoxic; hypotensive; anti-thyroid; anti-inflammatory; immunomodulator; dermatological; analgesic; viricide; antibacterial; fungicide.
XX	OS Homo sapiens.
XX	PN WO20190366-A2.
XX	29-NOV-2001.
DR	WPI: 2001-639362/76.
XX	N-PSDB; ABN75477.
PT	Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.
PT	Claim 10; Page 971-972; 2508pp; English.
XX	CC
CC	Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF-ORF534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haemopoiesis regulation, receptor/ligand, antiinflammatory activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, tissue growth, angiogenesis, activin or inhibitor activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce protein, which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
XX	SO
Query Match	85.7%; Score 234; DB 23; Length 104;
Best Local Similarity	84.9%; Pred. No. 4.4e-27;
Matches	45; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy	1 KOPRKKRGRYRQYDHEIMEAIAAMVMSKMSVSKAQGIGYVPHSTLEYVKVER 53
Db	8 KOPRKKRGRYRQYDHEIMEAIAAMVMSKMSVSKAQGIGYVPHSTLEYVKVER 60
RESULT 5	
AB24593	Matches 45; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
ID	AB24593 standard; Protein: 54 AA.
AC	AB24593;
XX	DT 04-OCT-2002 (first entry)
XX	XX

DE Fish E93 programmed cell death modulating protein conserved domain.

XX

KW Fish; cancer; programmed cell death modulating protein; adenocarcinoma; cellular apoptosis; leukaemia; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; Alzheimer's disease; retinitis pigmentosa; Parkinson's disease; myelodysplastic syndrome; cerebellar degeneration; aplastic anaemia; ischaemic injury; myocardial infarction; stroke; reperfusion injury; toxin-induced disease; genetic immunodeficiency; vaccine; gene therapy; lymphoma; cytostatic; melanoma; neuroprotective; myeloma; nootropic; vasotropic; immunostimulant; cerebroprotective; cardiant; E93 protein.

XX

Tetraodon nigroviridis.

OS

W0200234882-A2.

PN

XX

PD

02-MAY-2002.

XX

PP 29-OCT-2001; 2001WO-US48053.

XX

PR 27-OCT-2000; 2000US-243865P.

XX

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX

PI Baehrecke EH;

XX

DR WPI; 2002-479717/51.

XX

PT Novel programmed cell death modulating proteins, useful for treating or preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction.

XX

PS Claim 1; Fig 1; 88pp; English.

XX

CC The present invention relates to novel programmed cell death modulating proteins and polynucleotides encoding such proteins. Sequences of the invention are useful to screen potential cellular apoptosis inhibiting compounds to determine their use as therapeutic agents for treatment of diseases associated with increased programmed cell death. They are also useful for treating or preventing disorders associated with decrease in apoptosis. Programmed cell death modulating sequences are useful for treating or preventing cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma. Inhibition of the activity of the sequences of the invention are useful for treating disorders associated with increase in cell death or apoptosis such as acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g., Alzheimer's disease, retinitis pigmentosa, Parkinson's disease and cerebellar degeneration), ischaemic injuries (e.g., myocardial infarction, stroke, reperfusion injury), myelodysplastic syndromes (e.g., aplastic anaemia), toxin-induced diseases and other infectious or genetic immunodeficiencies. Sequences of the invention are used as vaccines and in gene therapy. The present sequence is fish E93 programmed cell death modulating protein conserved domain.

XX

SQ Sequence 54 AA:

Query Match 85.5%; Score 233.5; DB 23; Length 54;
Best Local Similarity 81.5%; Pred. No. 2.e-27; Matches 44; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

Qy 1 KOPRKRRGRYQDYHEIMEA-TIAMMGSKMSVSKAQGIVGVPHSLEVKYKER 53
Db 1 KOPRKRRGRYQDYHEIMEA-TIAMMGSKMSVSKAQGIVGVPHSLEVKYKER 54

RESULT 6

AAE24594
ID AAE24594 standard; Protein; 53 AA.

XX

AC AAE24594;

XX

DT 04-OCT-2002 (first entry)

XX

DE Mouse E93 programmed cell death modulating protein conserved domain.

XX

KW Mouse; cancer; programmed cell death modulating protein; adenocarcinoma; cellular apoptosis; leukaemia; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; Alzheimer's disease; retinitis pigmentosa; Parkinson's disease; myelodysplastic syndrome; cerebellar degeneration; aplastic anaemia; ischaemic injury; myocardial infarction; stroke; reperfusion injury; toxin-induced disease; genetic immunodeficiency; vaccine; gene therapy; lymphoma; cytostatic; melanoma; neuroprotective; myeloma; nootropic; vasotropic; immunostimulant; cerebroprotective; cardiant; E93 protein.

XX

OS Mus musculus.

XX

W0200234882-A2.

XX

PD 02-MAY-2002.

XX

PP 29-OCT-2001; 2001WO-US48053.

XX

PR 27-OCT-2000; 2000US-243865P.

XX

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX

PI Baehrecke EH;

XX

DR WPI; 2002-479717/51.

XX

PT Novel programmed cell death modulating proteins, useful for treating or preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction.

XX

PS Claim 1; Fig 1; 88pp; English.

XX

CC The present invention relates to novel programmed cell death modulating proteins and polynucleotides encoding such proteins. Sequences of the invention are useful to screen potential cellular apoptosis inhibiting compounds to determine their use as therapeutic agents for treatment of diseases associated with increased programmed cell death. They are also useful for treating or preventing disorders associated with decrease in apoptosis. Programmed cell death modulating sequences are useful for treating or preventing cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma. Inhibition of the activity of the sequences of the invention are useful for treating disorders associated with increase in cell death or apoptosis such as acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g., Alzheimer's disease, retinitis pigmentosa, Parkinson's disease and cerebellar degeneration), ischaemic injuries (e.g., myocardial infarction, stroke, reperfusion injury), myelodysplastic syndromes (e.g., aplastic anaemia), toxin-induced diseases and other infectious or genetic immunodeficiencies. Sequences of the invention are used as vaccines and in gene therapy. The present sequence is mouse E93 programmed cell death modulating protein conserved domain.

XX

SQ Sequence 53 AA:

Query Match 83.9%; Score 229; DB 23; Length 53;
Best Local Similarity 81.1%; Pred. No. 1e-26; Matches 43; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KOPRKRRGRYQDYHEIMEA-TIAMMGSKMSVSKAQGIVGVPHSLEVKYKER 53
Db 1 KOPRKRRGRYQDYHEIMEA-TIAMMGSKMSVSKAQGIVGVPHSLEVKYKER 53

RESULT 7

AAE24370
ID AAE24370 standard; Protein; 53 AA.

XX

AC AAE24370;

XX

DT	04-OCT-2002	(first entry)
XX	DE	Fruit fly E93 programmed cell death modulating protein conserved domain.
XX	DE	Fruit fly; programmed cell death modulating protein; adenocarcinoma; cellular apoptosis; leukaemia; acquired immunodeficiency syndrome; AIDS; neurodegenerative disease; Alzheimer's disease; retinitis pigmentosa; Parkinson's disease; myelodysplastic syndrome; cerebellar degeneration; aplastic anaemia; ischaemic injury; myocardial infarction; stroke; reperfusion injury; toxin-induced disease; genetic immunodeficiency; vaccine; gene therapy; lymphoma; cytostatic; melanoma; neuroprotective; myeloma; nontropic; vasotropic; immunostimulant; cerebroprotective; cardiotropic; cancer; E93 protein.
XX	OS	Drosophila melanogaster.
XX	PF	Drosophila melanogaster polypeptide SEQ ID NO 40227.
XX	PN	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
XX	PD	W0200171042-A2.
XX	PD	27-SEP-2001.
XX	XX	Drosophila melanogaster.
XX	XX	29-OCT-2001; 2001WO-US48053.
XX	XX	27-OCT-2000; 2000US-243855P.
XX	PA	(UYMA-) UNTV MARYLAND BIOTECHNOLOGY INST.
XX	PA	PI Baehrecke EH;
XX	DR	WPI: 2002-479717/51.
XX	PT	Novel programmed cell death modulating proteins, useful for treating or preventing disorders associated with abnormal cell proliferation and apoptosis such as cancer, stroke, Parkinson's disease, myocardial infarction
XX	PT	Claim 1; Fig 1; 88pp; English.
XX	PT	The present invention relates to novel programmed cell death modulating proteins and polynucleotides encoding such proteins. Sequences of the invention are useful to screen potential cellular apoptosis inhibiting compounds to determine their use as therapeutic agents for treatment of diseases associated with increased programmed cell death. They are also useful for treating or preventing disorders associated with decrease in apoptosis. Programmed cell death modulating sequences are useful for treating or preventing cancer e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma. Inhibition of the activity of the sequences of the invention are useful for treating disorders associated with increase in cell death or apoptosis such as acquired immunodeficiency syndrome (AIDS), neurodegenerative diseases (e.g., Alzheimer's disease, retinitis pigmentosa, Parkinson's disease and cerebellar degeneration), ischaemic injuries (e.g., myocardial infarction, stroke, reperfusion injury), myelodysplastic syndromes (e.g., aplastic anaemia), toxin-induced diseases and other infectious or genetic immunodeficiencies. Sequences of the invention are used as vaccines and in gene therapy. The present sequence is fruit fly E93 programmed cell death modulating protein
CC	CC	102(2) 7
CC	CC	Sequence 1140 AA;
CC	CC	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 23; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-17; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	XX	PS Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5777-ABB7207).
CC	CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences .
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
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CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
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CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
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CC	XX	PAEKE) PE CORP NY.
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CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9
CC	CC	Query Match 60.4%; Score 165; DB 22; Length 1140; Best Local Similarity 60.4%; Pred. No. 2.4e-15; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
CC	CC	Qy 1 KOPRKKRGRYRQDHEIMEEAIAVMMSGKMSVSKAOQIYGVPHTLEYKVKE 53
CC	CC	Db 741 KGTRPKRGKRYNDRDSLVEAVAKVQRGEMSVHRAGSYVGVPHSTLEYKVKE 793
CC	CC	RESULT 9
CC	CC	AAE24372
CC	CC	AAE24372 Standard; Protein: 1165 AA.
CC	CC	04-OCT-2002 (first entry)
CC	DE	Fruit fly E93 programmed cell death modulating protein #1.
CC	XX	W0200171042-A2.
CC	AC	23-MAR-2001; 2001WO-US09231.
CC	PR	23-MAR-2000; 2000US-191637P.
CC	PR	11-JUL-2000; 2000US-0614150.
CC	PA	(PEKE) PE CORP NY.
CC	PA	WPI: 2001-656860/75.
CC	DR	N-PSDB; ABL15248.
CC	XX	PAEKE) PE CORP NY.
CC	XX	WPI: 2001-656860/75.
CC	XX	PI Venter JC, Adams M, Li PWD, Myers EW;
CC	XX	DR
CC	PS	Disclosure; SEQ ID NO 40227; 21pp + sequence Listing; English.
CC	XX	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.
CC	XX	Sequence 1140 AA;
CC	XX	RESULT 9

GenCore version 5.1.6									
Copyright (c) 1993 - 2003 Compugen Ltd.									
OM protein - protein search, using sw model									
Run on: August 4, 2003, 15:01:44 ; Search time 95 seconds									
(without alignments)									
143.966 Million cell updates/sec									
Title: US-10-016-768a-2	17	69.5	25.5	1046	5	09w0w2	03w0w2 drosophila	03w0w2 drosophila	
Perfect score: 273	18	69	25.3	365	3	09p3f3	09p3f3 neurospora	09p3f3 neurospora	
Sequence: 1 KQPRKKRGRYROYDHEIMEE.....KAQSIYGVPHSTLEYKVKER 53	19	67	24.5	924	16	08cjl0	08cjl0 streptomyces	08cjl0 streptomyces	
Scoring table: BL0SUM62	20	64	23.4	393	11	08c9j6	08c9j6 mus musculus	08c9j6 mus musculus	
Gapop 10.0 , Gapext 0.5	21	63	23.1	977	5	09w0k7	09w0k7 drosophila	09w0k7 drosophila	
Searched: 830525 seqs, 25052604 residues	22	63	23.1	979	5	09j1h7	09j1h7 drosophila	09j1h7 drosophila	
Total number of hits satisfying chosen parameters: 830525	23	61	22.3	478	16	08r5t4	08r5t4 thermomoanaer	08r5t4 thermomoanaer	
Minimum DB seq length: 0	24	61	22.3	494	16	08s5h9	08s5h9 streptococcus	08s5h9 streptococcus	
Maximum DB seq length: 2000000000	25	61	22.3	494	16	08z2t2	08z2t2 streptococcus	08z2t2 streptococcus	
Post-processing: Minimum Match 0%	26	60.5	22.2	325	3	09uwg7	09uwg7 magnaporthe	09uwg7 magnaporthe	
Listing first 45 summaries	27	59.5	21.8	267	5	09g27	09g27 drosophila	09g27 drosophila	
database : SPTREMBL 23:*	28	59	21.8	257	5	09j5yx7	09j5yx7 drosophila	09j5yx7 drosophila	
1: sp_archea:*	29	59.5	21.8	551	8	09m164	09m164 beta vulgaris	09m164 beta vulgaris	
2: sp_bacteria:*	30	59	21.6	176	2	08keb4	08keb4 enterococcus	08keb4 enterococcus	
3: sp_fungi:*	31	59	21.6	308	15	08pcx8	08pcx8 xanthomonas	08pcx8 xanthomonas	
4: sp_human:*	32	59	21.6	342	16	08f5p1	08f5p1 leprosophila	08f5p1 leprosophila	
5: sp_invertebrate:*	33	59	21.6	419	2	044445	016445 chlamydia t	016445 chlamydia t	
6: sp_mammal:*	34	59	21.6	424	15	084654	084654 chlamydia t	084654 chlamydia t	
7: sp_mhc:*	35	59	21.6	470	13	08qcw1	08qcw1 anguilla ja	08qcw1 anguilla ja	
8: sp_organelle:*	36	59	21.6	1057	5	09u1h3	09u1h3 drosophila	09u1h3 drosophila	
9: sp_phage:*	37	58.5	21.4	224	2	08vwq3	08vwq3 staphylococcus	08vwq3 staphylococcus	
10: sp_plant:*	38	58.5	21.4	224	2	08gfr0	08gfr0 staphylococcus	08gfr0 staphylococcus	
11: sp_primate:*	39	58.5	21.4	224	2	08gwm8	01g8w8 staphylococcus	01g8w8 staphylococcus	
12: sp_virus:*	40	58	21.2	193	4	08n9y1	08n9y1 homo sapiens	08n9y1 homo sapiens	
13: sp_vertebrate:*	41	58	21.2	271	17	08tmt7	08tmt7 mettisarcus	08tmt7 mettisarcus	
14: sp_unclassified:*	42	58	21.2	306	16	08g612	08pg12 xanthomonas	08pg12 xanthomonas	
15: sp_rvirus:*	43	58	21.2	413	4	08tlf9	08tlf9 homo sapiens	08tlf9 homo sapiens	
16: sp_bacteriopl:*	44	58	21.2	761	16	08dia17	08dia17 synchococcus	08dia17 synchococcus	
17: sp_archeap:*	45	58	21.2	1880	5	018465	018465 hirudo medinella	018465 hirudo medinella	
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query	Match Length	DB	ID	Description	RESULT 1		
							ID: Q96nk1	PRELIMINARY:	PRT: 213 AA.
1	273	100.0	213	4	Q96nk1	Q96nk1 homo sapiens	AC: Q96nk1;		
2	273	100.0	517	11	Q8cjj4	Q8cjj4 mus musculus	DT: 01-DEC-2001 (TREMBLrel. 19, Created)		
3	242	88.6	396	11	Q8cq90	Q8cq90 mus musculus	DT: 01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
4	242	88.6	433	11	Q8bg72	Q8bg72 mus musculus	DT: 01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
5	242	88.6	4	Q96jno	Q96jno homo sapiens	DE: Hypothetical protein FLJ30596.			
6	242	88.6	619	4	Q8h3l6	Q8h3l6 homo sapiens	DS: Homo sapiens (Human).		
7	165	60.4	1165	5	Q9vd60	Q9vd60 drosophila	DS: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
8	165	60.4	198	5	Q93ym8	Q93ym8 apis mellifera	DS: NCBI_TaxID=9606;		
9	163	59.7	185	5	Q22051	Q22051 caenorhabditis	DS: [1]		
10	88.5	32.4	645	5	Q8mkx3	Q8mkx3 drosophila	RP: TISSUE-Brain;		
11	88.5	32.4	660	5	Q24457	Q24457 drosophila	RA: Tashiro H., Yamazaki M., Matanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiya M., Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahashi K., Masuho Y., Nagai K., Isogai T.		
12	88.5	32.4	1064	5	Q9v5n1	Q9v5n1 drosophila	RA: "NEDO human cDNA sequencing project.";		
13	88.5	32.4	1085	5	Q24455	Q24455 drosophila	RA: Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
14	78.5	28.8	652	5	Q7168	Q7168 apis mellifera	RA: DR: AK05258; BAB10892.1; -		
15	72	26.4	107	12	Q91ih0	Q91ih0 frog adanov	RA: KW: Hypothetical protein.		
16	70.5	25.8	661	5	Q9v8s2	Q9v8s2 drosophila	RA: SEQUENCE 213 AA; 23477 MW; 4D7F6CABF95251B2 CRC64;		
ALIGNMENTS									
Query	Match Length	DB	ID	Description	Query	Match Length	100.0%	Score 273;	DB 4;
									Length 213;
									Best Local Similarity 100.0%;
									Pred. No. 2.4e-6;
									Matches 53; Conservative 0;
									Mismatches 0;
									Indels 0;
									Gaps 0;

Q8CG44 PRELIMINARY; PRT; 517 AA.
 ID Q8CG44
 AC Q8CG44;
 DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)
 DE Transcription factor MLR1.
 GN MLR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Kunieda T., Park J., Takeuchi H., Kubo T.;
 RT "Mus musculus mrl1 and mrl2 mRNA for transcription factor MLR1 and MLR2.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB76070; BAC20954.1; -.
 SQ SEQUENCE 517 AA; 57316 MW; C97403D3D296C52E CRC64;
 Query Match 100.0%; Score 273; DB 11; Length 517;
 Best Local Similarity 100.0%; Pred. No. 6.4e-26;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 53
 Db 429 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 481

RESULT 3
 Q8C900 PRELIMINARY; PRT; 396 AA.
 ID Q8C900
 AC 08C900
 DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE-2003 (TREMBrel. 23, Last annotation update)
 DR EMBL; AB041621; BAC30816.1; -.
 SQ SEQUENCE 396 AA; 47124 MW; 736656D1F7E9A041 CRC64;
 Query Match 88.6%; Score 242; DB 11; Length 433;
 Best Local Similarity 86.8%; Pred. No. 4.2e-22;
 Matches 46; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 53
 Db 337 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 389

RESULT 5
 Q96JN0 PRELIMINARY; PRT; 572 AA.
 ID Q96JN0
 AC 096JN0;
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-OCT-2002 (TREMBrel. 22, Last annotation update)
 DE Hypothetical protein KIR1795 (Fragment).
 GN KIR1795.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE-21245130; PubMed=11347905;
 RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of 100 new cDNA clones from brain which code for large Proteins in vitro.";
 RT DNA Res. 8:85-95 (2001).
 RL DR EMBL; AB058698; BAA47424.1; -.
 KW Hypothetical protein.
 FT NON-TER 396 AA; 43085 MW; EEA4A585F62336E35 CRC64;
 SQ SEQUENCE 396 AA; 43085 MW; EEA4A585F62336E35 CRC64;
 Query Match 88.6%; Score 242; DB 11; Length 396;
 Best Local Similarity 86.8%; Pred. No. 3.8e-22;
 Matches 45; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 53
 Db 337 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 389

RESULT 4
 Q8BGT2 PRELIMINARY; PRT; 433 AA.
 ID Q8BGT2
 AC 08BGT2
 DT 01-MAR-2003 (TREMBrel. 23, Created)
 DT 01-MAR-2003 (TREMBrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBrel. 23, Last annotation update)
 DR 01-MAR-2003 (TREMBrel. 23, Last annotation update)

DE Transcription factor MLR2 (Hypothetical protein).
 GN MLR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Kunieda T., Park J., Takeuchi H., Kubo T.;
 RT "Mus musculus mrl1 and mrl2 mRNA for transcription factor MLR1 and MLR2.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB076070; BAC20954.1; -.
 SQ SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Kunieda T., Park J., Takeuchi H., Kubo T.;
 RT "Mus musculus mrl1 and mrl2 mRNA for transcription factor MLR1 and MLR2.";
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RT Nature 420:563-573 (2002).
 DR EMBL; AB076070; BAC20955.1; -.
 DR EMBL; AK041609; BAC30816.1; -.
 DR EMBL; AK041609; BAC30816.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 433 AA; 47124 MW; 736656D1F7E9A041 CRC64;
 Query Match 88.6%; Score 242; DB 11; Length 433;
 Best Local Similarity 86.8%; Pred. No. 4.2e-22;
 Matches 46; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 53
 Db 337 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 389

RESULT 6
 QY 1 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 53
 Db 476 KOPRKKRGRYRQYDHEIMERAIAMVMSGKMSVSKAQGIVGVPHSTLEYKVKER 528

ID	NAME	PRELIMINARY	PRT;	619 AA.
08N316				
08N316;	AC			
01-OCT-2002	(TREMBLrel. 22, Created)			
01-OCT-2002	(TREMBLrel. 22, Last sequence update)			
01-OCT-2002	(TREMBLrel. 22, Last annotation update)			
DE	Hypothetical protein (Fragment)			
GN	Homo sapiens (Human)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	wambutt R., Heubner D., Mewes H.W., Weil B., Wiemann S.,			
RL	Submitted (JUL 2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; ALB34245; CAD38921; 1; -.			
KW	Hypothetical protein.			
FT	NON-TER 1			
SEQUENCE	619 AA; 67378 MW; 791286EC6F8A5110 CRC64;			
Query Match	88.6%; Score 242; DB 4; Length 619;			
Best Local Similarity	86.8%; Pred. No. 6.3e-22;			
Matches	46; Conservative 5; Mismatches 2; Indels 0; Gaps 0;			
Qy	1 KOPRKKGRRYQDHEMEEATAMVMSKMSVSKAQGIGYGVPHSTLEYKVER 53			
Db	523 KOPRKKGRRYQDHEMEEATAMVMSKMSVSKAQGIGYGVPHSTLEYKVER 575			
RESULT	7			
ID	09V600	PRELIMINARY;	PRT;	1165 AA.
AC	09V600;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAY-2003 (TREMBLrel. 23, Last annotation update)			
DE	CG18389 protein			
GN	EP193F OR CG18389.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydriidae; Drosophilidae; Drosophila.			
OX	NCBI_TAXID=7277;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Berkeley;			
RX	MEDLINE-20196006; PubMed-10731132;			
RA	Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,			
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,			
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
RA	Sutcliffe G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,			
RA	Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			
RA	Wan K.H., Doyle C., Baxter E.G., Holt G., Nelson C.R., Miklos G.L.G.,			
RA	Abrial J.F., Agbayani A., An H.-J., Andrews-Pannoch C., Baldwin D.,			
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,			
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boisshakov S.,			
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			
RA	Burkis J.C., Busam D.A., Dahlke C., Cadieu E., Center A., Chandra I.,			
RA	Cherry J.M., Cawley D., Dahlke C., Davenport L.B., Davies P.,			
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			
RA	Durbin R.M., Ewing B., Evans C., Ferrer J., Fierro J., Flanagan J.,			
RA	Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,			
RA	Gloedk A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			
RA	Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,			
RA	Houston K.A., Houston T.J., Holand T.J., Wei M.-H., Ibegwam C.,			
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,			
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,			
RA	Merkulov G., Milashina N.V., Mobarie C., Morris J., Moshrefi A.,			
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzzey D.M., Nelson D.L.,			
RESULT	8			
ID	095Y8	PRELIMINARY;	PRT;	1598 AA.
AC	095Y8;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DE	MBLK-1 protein.			
GN				
OS	Euphydryas mellifera (Honeybee).			

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7460;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=21873258; PubMed=11881813;
 RA TAKEUCHI H., Kage E., Sawata M., Kanikouchi A., Ohashi K., Ohara M.,
 RA FUJIYUKI T., Kunieda T., Sekimizu K., Natori S., Kubo T.;
 RT "Identification of a novel gene, Mbik-1, that encodes a putative
 RT transcription factor expressed preferentially in the large-type Kenyon
 RT cells of the honey bee brain."
 RL Insect Mol Biol. 10:487-504 (2001).
 DR EMBL: AB04034; BAB64310.1;
 SQ SEQUENCE 1598 AA; 174929 MW; E5475BDD3ACB1EEF CRC64;

Query Match 60.4%; Score 165; DB 5; Length 1598;
 Best Local Similarity 60.4%; Pred. No. 9 3e-12;
 Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;
 Qy 1 KQPRKKRKRQYQDHETMEIAIAMVMSGKMSVSKAOGIYGVPHSTLEYKVER 53
 Db 1031 KGTTRPKRGKRYNDRDSLVEAVRAVORGEMSVHRAGSYGVPHSTLEYKVER 1083

RESULT 9
 Q22051 PRELIMINARY; PRT; 185 AA.
 AC 022051;
 DT 01-NOV-1996 (TREMBREL, 01, Last sequence update)
 DT 01-MAR-2003 (TREMBREL, 23, Last annotation update)
 DE T01C1.3. protein.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrine; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N_A.
 RA Leonard N.;
 RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N_A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode *C.elegans*: A platform for
 investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL: 268010; CAA93009.1; -.
 DR WormPep; T01C1.3; CE03594;
 SQ SEQUENCE 185 AA; 20706 MW; F9759327B318F641 CRC64;

Query Match 59.7%; Score 163; DB 5; Length 185;
 Best Local Similarity 56.6%; Pred. No. 1.5e-12;
 Matches 30; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 Qy 1 KOPRKKRKRQYQDHETMEIAIAMVMSGKMSVSKAOGIYGVPHSTLEYKVER 53
 Db 83 KRSRPRKGQYKDVNALDEAVRSVFRGEMVHFRAGSFFGVPHSTLEYKVER 135

RESULT 10
 Q8MKX3 PRELIMINARY; PRT; 645 AA.
 AC 08MKX3;
 DT 01-OCT-2002 (TREMBREL, 22, Created)
 DT 01-MAR-2003 (TREMBREL, 23, Last sequence update)
 DE CG2368-CPD;
 GN PSQ OR CG2368.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydriidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N_A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfleiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boishakow S.,
 RA Borko D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler C., Cadile E., Center A., Chandra I.,
 RA Cherry J.M., Cowley S., Dahake R., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeawam C.,
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Koide C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moharry C., Morris J., Mosherfi A.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Nelson D.M., Murphy B., Murphy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zha Q., Zheng L.,
 RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:218-2195(2000).
 RN [2]
 RP SEQUENCE FROM N_A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Carlson J.W., Baldwin J., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Baldwin J., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champie M., Davenport L.B., Diez S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresneak D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibedawam C., Jallali M., Kruse D., Li P., Mattei B., Mosherfi A.,
 RA McIntosh T.C., Moy M., Murphy B., Murphy D.M., Nelson K.A., Nunoo J.,
 RA Parcileb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stiplton M., Strong R., Svirkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of the *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N_A.
 RA Misra S., Crosty M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnicki F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.B.;
 RT "Annotation of *Drosophila melanogaster* genome."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

DR FlyBase; FBgn004399; psq.

DR InterPro; IPR002110; BTB_PoZ.

DR InterPro; IPR002117; HTH_Fis.

DR Pfam; PF00651; BTB; 1.

DR SMART; SM00225; BTB; 1.

DR TIGRFAMS; TIGR01199; HTH_fis; 2.

DR PROSITE; PS50097; BTB; 1.

KW Alternative splicing.

FT 1 429 MISSING (IN ISOFORM B).

FT VARSPLC 719 736 MISSING (IN ISOFORM 2).

FT CONFLICT 1020 1020 Q -> QO (IN RBF. 1 AND 2).

SQ SEQUENCE 1064 AA; 114984 MW; 7740C782DE6ECA5 CRC64;

Query Match 32.4%; Score 88.5; DB 5; Length 1064; Best Local Similarity 34.7%; Pred. No. 0.027; Matches 17; Conservative 14; Mismatches 17; Indels 1; Gaps 1; Matches 17; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

OY 5 KRRGRYROYDHMEATAMVMSKMSVSKAQIYGIVPHSTLEYKKVER 53

Db 773 KKEGGTKSWNEDALQNALEARLSQGQISANKASKAFGIPSSYL-YKARR 820

RESULT 13

Q24455 PRELIMINARY; PRT; 1085 AA.

ID 024455; Q24456; Q24003; RC

AC 024455; Q24456; Q24003; ID 077168 PRELIMINARY; PRT; 652 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created) AC 077168;

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update) DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update) DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Pipsqueak protein (BTB-V protein domain). DE Pipsqueak.

GN PSQ OR CG2368. OS apis mellifera (Honeybee).

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; OC Apidae; Apis.

OC NCBI_TaxID:7460; OX

RN [1] RP SEQUENCE FROM N.A.

RX TISSUE:Brain; RX MEDLINE=98447711; PubMed=974480;

RA Lehmann M., Siegmund T., Lintermann K.G.; Korge G.; RA Lehmann M., Siegmund T., Lintermann K.G.; Korge G.;

RT "The pipsqueak protein of Drosophila melanogaster binds to GAGA sequences through a novel DNA-binding domain"; RT "The pipsqueak protein of Drosophila melanogaster binds to GAGA sequences through a novel DNA-binding domain";

RL J. Biol. Chem. 273:28504-28509(1998). DR AF08456; ACT1015; 1.

DR AF08456; ACT1015; 1.

DR InterPro; IPR002110; BTB_PoZ.

DR InterPro; IPR002117; HTH_Fis.

DR Pfam; PF0051; BTB; 1.

DR SMART; SM00225; BTB; 1.

DR TIGRFAMS; TIGR01199; HTH_fis; 2.

DR PROSITE; PS50097; BTB; 1.

SQ SEQUENCE 652 AA; 71787 MW; 72984B3379454164 CRC64;

Query Match 28.8%; Score 78.5; DB 5; Length 652; Best Local Similarity 34.7%; Pred. No. 0.28; Matches 17; Conservative 11; Mismatches 20; Indels 1; Gaps 1; Matches 17; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

OY 5 KRRGRYROYDHMEATAMVMSKMSVSKAQIYGIVPHSTLEYKKVER 53

Db 457 KKDQGPKSWDESLNALDKRGTISANKASKAFGIPSSYL-YKARR 504

RESULT 15

Q91HO0 PRELIMINARY; PRT; 107 AA.

ID Q91HO0; AC Q91HO0;

DT 01-OCT-2000 (TREMBLrel. 15, Created) DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE 22K protein.

OS Frog adenovirus 1.

OS Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Siadenovirus.

OX NCBI_TaxID:114102;

RN [1] RP SEQUENCE FROM N.A.

RX MEDLINE=20451109; PubMed=10993931;

RA Davidson A.J., Wright K.M., Harrach B.; RA DNA sequence of frog adenovirus.;

RL J. Gen. Virol. 81:2431-2439(2000).

RA [2] SEQUENCE FROM N.A.

RA Davidson A.J., Wright K.M., Harrach B.; RA Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBB; AF224336; AF86336.1; .

SQ SEQUENCE 107 AA; 12150 MW; 22B1E385139CA157 CRC64;

Mon Aug 4 16:28:25 2003

us-10-016-768a-2.rspt

Page 7

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Best Local Similarity 33 3%; Pred. No. 0.24;
Matches 19; Conservative 15; Mismatches 17; Indels 6; Gaps 3;
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Db 31 KRRKVPGTVKKWKLHLGEIQEVMAIVGASTKSVKRLLETKGI-NIPGSTINYVK 86

Search completed: August 4, 2003, 15:06:47
Job time : 100 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 15:06:54 ; Search time 50 Seconds

(without alignments)

125.885 Million cell updates/sec

Title: US-10-016-768a-2

Perfect score: 273

Sequence: 1 KOPRKRRGRYRQYDHIMEEE... KAOQIYGVPHSTLEYVKER 53

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 11875970 residues

total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	273	100.0	442	14	US-10-016-768-8
3	233.5	85.5	54	14	US-10-016-768-3
4	229	83.9	53	14	US-10-016-768-4
5	165	60.4	53	14	US-10-016-768-1
6	165	60.4	1165	14	US-10-016-768-10
7	163	59.7	53	14	US-10-016-768-5
8	66	24.2	378	15	US-10-16-761-12022
9	62	22.7	325	11	US-09-938-901-2
10	61	22.3	352	9	US-09-741-669-432
11	58	21.2	364	9	US-03-886-400-4
12	58	21.2	364	14	US-10-112-357-4
13	58	21.2	364	14	US-10-114-403-4
14	58	21.2	364	14	US-10-116-506-4
15	58	21.2	364	14	US-10-112-331-4

ALIGNMENTS

RESULT 1

US-10-016-768-2

; Sequence 2, Application US/10016768-
; Publication No. US2002142443A1

; GENERAL INFORMATION:

; APPLICANT: Baehrcke, Eric H.

; TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH

; FILE REFERENCE: 4115-131

; CURRENT APPLICATION NUMBER: US/10/016,768

; CURRENT FILING DATE: 2001-10-29

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin version 3.1

; SEQ ID NO: 2

; LENGTH: 53

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: C

; NAME/KEY: MISC-FEATURE

; LOCATION: (1)..(54)

; OTHER INFORMATION: X CAN BE ANY AMINO ACID

US-10-016-768-2

Query Match 100.0% ; Score 273; DB 14; Length 53;

Best Local Similarity 100.0%; Pred. No. 3; 6e-31; 0; Mismatches 0; Indels 0; Gaps 0;

Matches 53; Conservative 0; Sequence 1, Appli

QY 1 KOPRKRRGRYRQYDHIMEEEIAAMVMSGKMSVSKAQGIYGVPHSTLEYVKER 53

Db 1 KOPRKRRGRYRQYDHIMEEEIAAMVMSGKMSVSKAQGIYGVPHSTLEYVKER 53

RESULT 2

US-10-016-768-8

; Sequence 4, Appli

; Sequence 8, Application US/10016768

; Publication No. US2002142443A1

; GENERAL INFORMATION:

; APPLICANT: Baehrcke, Eric H.

; TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH

FILE REFERENCE: 4115-131
 CURRENT APPLICATION NUMBER: US/10/016/768
 CURRENT FILING DATE: 2001-10-29
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 8
 LENGTH: 442
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-016-768-8

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 Best Local Similarity 100.0%; Pred. No. 5.2e-30; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 353 KOPRKKGRRQYDHEIMERAIAAMVMSKMSVSKAQGIVGVPHSTLEYVKER 405

RESULT 3
 US-10-016-768-3
 Sequence 3, Application US/10016768
 Publication No. US20020142443A1
 GENERAL INFORMATION:
 APPLICANT: Baehrecke, Eric H.
 TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH
 FILE REFERENCE: 4115-131
 CURRENT APPLICATION NUMBER: US/10/016/768
 CURRENT FILING DATE: 2001-10-29
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 3
 LENGTH: 54
 TYPE: PRT
 ORGANISM: T. nigroviridis
 US-10-016-768-3

Query Match 85.5%; Score 233.5; DB 14; Length 54;
 Best Local Similarity 81.5%; Pred. No. 1.3e-25; Matches 44; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

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 Db 1 KOPRKKGRRQYDHEIMERAIAAMVMSKMSVSKAQGIVGVPHSTLEYVKER 54

RESULT 4
 US-10-016-768-4
 Sequence 4, Application US/10016768
 Publication No. US20020142443A1
 GENERAL INFORMATION:
 APPLICANT: Baehrecke, Eric H.
 TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH
 FILE REFERENCE: 4115-131
 CURRENT APPLICATION NUMBER: US/10/016/768
 CURRENT FILING DATE: 2001-10-29
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 10
 LENGTH: 1165
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-10-016-768-10

Query Match 60.4%; Score 165; DB 14; Length 53;
 Best Local Similarity 60.4%; Pred. No. 5.6e-16; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 KOPRKKGRRQYDHEIMERAIAAMVMSKMSVSKAQGIVGVPHSTLEYVKER 53
 Db 1 KGTRPKRGKRYDSDLVEAVKAVORGEMSVRHAGSYGVPHSTLEYVKER 53

RESULT 5
 US-10-016-768-1
 Sequence 1, Application US/10016768
 Publication No. US20020142443A1
 GENERAL INFORMATION:
 APPLICANT: Baehrecke, Eric H.
 TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH
 FILE REFERENCE: 4115-131
 CURRENT APPLICATION NUMBER: US/10/016/768
 CURRENT FILING DATE: 2001-10-29
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 1
 LENGTH: 53
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)-(54)
 OTHER INFORMATION: X can be any amino acid
 US-10-016-768-1

Query Match 60.4%; Score 165; DB 14; Length 1165;
 Best Local Similarity 60.4%; Pred. No. 5.6e-14; Matches 32; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

QY 1 KOPRKKGRRQYDHEIMERAIAAMVMSKMSVSKAQGIVGVPHSTLEYVKER 53
 Db 758 KGTRPKRGKRYDSDLVEAVKAVORGEMSVRHAGSYGVPHSTLEYVKER 810

RESULT 7
 US-10-016-768-5
 Sequence 5, Application US/10016768
 Publication No. US20020142443A1
 GENERAL INFORMATION:
 APPLICANT: Baehrecke, Eric H.
 TITLE OF INVENTION: GENES REGULATING PROGRAMMED CELL DEATH
 FILE REFERENCE: 4115-131
 CURRENT APPLICATION NUMBER: US/10/016/768
 CURRENT FILING DATE: 2001-10-29

Query Match 83.9%; Score 229; DB 14; Length 53;
 Best Local Similarity 81.1%; Pred. No. 5.6e-25; Matches 43; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

NUMBER OF SEQ ID NOS: 12
 SOFTWARE: PatentIn version 3.1
 SEQ ID NOS: 5
 LENGTH: 53
 TYPE: PRT
 ORGANISM: *Caenorhabditis elegans*
 FEATURE:
 NAME/KEY: MISC_FEATURE
 LOCATION: (1)..(54)
 OTHER INFORMATION: X CAN BE ANY AMINO ACID
 US-10-016-768-5

Query Match 59.7%; Score 163; DB 14; Length 53;
 Best Local Similarity 56.8%; Pred. No. 1.e-15;
 Matches 30; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

RESULT 8
 US-10-156-761-12022
 Sequence 12022, Application US/10156761
 Publication No. US20030119018A1
 Db 1 KRSRPRQGYRKYDKNALDEAVRSVRGEMTVHRASSPFGVPHSTLEYKVKE 53

GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIVIKI
 APPLICANT: HATTORI, MASAHIRO
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

CURRENT APPLICATION NUMBER: US/10/156,761
 FILE REFERENCE: 249-262
 CURRENT FILING DATE: 2002-05-29
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 12022
 LENGTH: 378
 TYPE: PRT
 ORGANISM: *Streptomyces avermitillii*
 US-10-156-761-12022

Query Match 24.2%; Score 66; DB 15; Length 378;
 Best Local Similarity 36.4%; Pred. No. 0.55; DB 15; Length 378;
 Matches 12; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

RESULT 9
 US-09-938-901-2
 Sequence 2, Application US/09938901
 Publication No. US20030008291A1
 GENERAL INFORMATION:
 APPLICANT: Kuramitsu Seiki,
 APPLICANT: Yokoyama Shigevuki
 TITLE OF INVENTION: GENE ENCODING DNA REPAIR ENZYME
 FILE REFERENCE: PH-1261-US
 CURRENT APPLICATION NUMBER: US/09/938,901
 CURRENT FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: JP2001-47762
 PRIOR FILING DATE: 2001-02-23
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2

Query Match 22.7%; Score 62; DB 11; Length 325;
 Best Local Similarity 32.6%; Pred. No. 1.7; DB 11; Length 325;
 Matches 15; Conservative 8; Mismatches 9; Indels 14; Gaps 2;

RESULT 10
 US-09-741-669-432
 Sequence 432, Application US/09741669
 Patent No. US20020022718A1
 GENERAL INFORMATION:
 APPLICANT: Forsyth, R. Allyn
 APPLICANT: Ohlsen, Kari L.
 APPLICANT: Zyskind, Judith W.
 TITLE OF INVENTION: Genes identified as required for proliferation of *E. coli*
 FILE REFERENCE: EL17RA.009A
 CURRENT APPLICATION NUMBER: US/09/741,669
 CURRENT FILING DATE: 2000-12-19
 PRIOR APPLICATION NUMBER: US 60/173005
 PRIOR FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOS: 481
 SOFTWARE: FastB2Q for Windows Version 4.0
 SEQ ID NO 432
 LENGTH: 352
 TYPE: PRT
 ORGANISM: *Escherichia coli*
 US-09-741-669-432

Query Match 22.3%; Score 61; DB 9; Length 352;
 Best Local Similarity 28.8%; Pred. No. 2.5; DB 9; Length 352;
 Matches 17; Conservative 15; Mismatches 15; Indels 12; Gaps 3;

RESULT 11
 US-09-886-400-4
 Sequence 4, Application US/09886400
 Patent No. US20020045226A1
 GENERAL INFORMATION:
 APPLICANT: DIVERSA CORPORATION
 APPLICANT: Murphy, Dennis
 APPLICANT: Ried, John
 TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE
 FILE REFERENCE: DIVER120-4
 CURRENT APPLICATION NUMBER: US/09/886,400
 CURRENT FILING DATE: 2001-06-20
 PRIOR APPLICATION NUMBER: 09/619,032
 PRIOR FILING DATE: 2000-07-19
 PRIOR APPLICATION NUMBER: 09/407,806
 PRIOR FILING DATE: 1999-09-20
 PRIOR APPLICATION NUMBER: 08/613,220
 PRIOR FILING DATE: 1995-03-08
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 364
 TYPE: PRT
 ORGANISM: *Thermococcus alcaliphilus*
 US-09-886-400-4

Query Match 21.2%; Score 58; DB 9; Length 364;

Best Local Similarity 36.4%; Pred. No. 7; Mismatches 18; Indels 2; Gaps 1; Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1; Sequence 4, Application US/10112357

Publication No. US2002011099A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: Murphy, Dennis

APPLICANT: Ried, John

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH

FILE REFERENCE: DIVER1120-4

CURRENT APPLICATION NUMBER: US/10/112,357

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 09/886,400

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/619,032

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/407,806

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 08/613,220

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 364

TYPE: PRT

ORGANISM: Thermococcus alcaliphilus

US-10-112-357-4

RESULT 12

US-10-112-357-4

Best Local Similarity 36.4%; Pred. No. 7; Mismatches 18; Indels 2; Gaps 1; Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1; Sequence 4, Application US/10112357

Publication No. US2002011099A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: Murphy, Dennis

APPLICANT: Ried, John

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH

FILE REFERENCE: DIVER1120-4

CURRENT APPLICATION NUMBER: US/10/112,357

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 09/886,400

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/619,032

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/407,806

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 08/613,220

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 364

TYPE: PRT

ORGANISM: Thermococcus alcaliphilus

US-10-112-357-4

RESULT 13

US-10-114-403-4

Best Local Similarity 36.4%; Pred. No. 7; Mismatches 18; Indels 2; Gaps 1; Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1; Sequence 4, Application US/10114403

Publication No. US2002011510A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: Murphy, Dennis

APPLICANT: Ried, John

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH

FILE REFERENCE: DIVER1120-4

CURRENT APPLICATION NUMBER: US/10/114,403

CURRENT FILING DATE: 2002-04-01

PRIOR APPLICATION NUMBER: 09/886,400

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/619,032

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/407,806

PRIOR FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 08/613,220

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 364

TYPE: PRT

ORGANISM: Thermococcus alcaliphilus

US-10-114-403-4

RESULT 14

US-10-116-606-4

Best Local Similarity 36.4%; Pred. No. 7; Mismatches 18; Indels 2; Gaps 1; Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1; Sequence 4, Application US/10116606

Publication No. US20020119515A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: Murphy, Dennis

APPLICANT: Ried, John

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH

FILE REFERENCE: DIVER1120-4

CURRENT APPLICATION NUMBER: US/10/116,606

CURRENT FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: US/09/886,400

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/619,032

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/407,806

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 08/613,220

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 364

TYPE: PRT

ORGANISM: Thermococcus alcaliphilus

US-10-116-606-4

RESULT 15

US-10-112-331-4

Best Local Similarity 36.4%; Pred. No. 7; Mismatches 18; Indels 2; Gaps 1; Matches 16; Conservative 8; Mismatches 18; Indels 2; Gaps 1; Sequence 4, Application US/10112331

Publication No. US20020119550A1

GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION

APPLICANT: Murphy, Dennis

APPLICANT: Ried, John

TITLE OF INVENTION: ENZYMES HAVING ALPHA-GALACTOSIDASE ACTIVITY AND METHODS OF USE TH

FILE REFERENCE: DIVER1120-4

CURRENT APPLICATION NUMBER: US/10/112,331

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: US/09/886,400

PRIOR FILING DATE: 2001-06-20

PRIOR APPLICATION NUMBER: 09/619,032

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/407,806

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 08/613,220

PRIOR FILING DATE: 1996-03-08

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 364

TYPE: PRT

ORGANISM: Thermococcus alcaliphilus

US-10-114-403-4

US-10-112-331-4

Search completed: August 4, 2003, 15:15:50
Job time : 51 secs

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STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 100337

TO: Minh-Tam Davis
Location: CM-1/8A01/8E12
Art Unit: 1642
Monday, August 04, 2003

Case Serial Number: 10/016768

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Davis,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

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